STIC-Biotech/ChemLib

141606

From:

Bunner, Bridget

Sent:

Monday, January 03, 2005 12:49 PM

To: Subject: STIC-Biotech/ChemLib sequence search

Hi! I'd like a sequence search performed for case 10/086,177:

- 1. the amino acid sequence of SEQ ID NO: 12
- 2. the amino acid sequence of SEQ ID NO: 13

Thanks!

Bridget Bunner

Art Unit 1647 Rem 4C65 (571) 272-0881 mailbox 4C70

STAFF USE ONLY

Searcher:

Searcher Phone: 2-

Date Searcher Picked up Date Completed:

Searcher Prep/Rev. Time:

Online Time:_

Type of Search

NA Sequence: #_

AA Sequence:#

Structure: #

Bibliographic:

Litigation:

Patent Family:

Other:

******** Vendors and cost where applicable

STN:_

DIALOG:

QUESTEL/ORBIT:

LEXIS/NEXIS:

SEQUENCE SYSTEM:

WWW/Internet:_

Other(Specify):_

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Minimum |
Maximum |
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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                                60.5
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seq length: 2000000000
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1 KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN
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   Issued_Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/pcTUS_COMB.pep:*

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Copyright (c) 1993 - 2005
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US-08-132-084A-1
US-08-461-912A-46
US-09-461-912A-46
US-08-323-084A-5
US-08-464-08-5
US-09-312-283C-421
US-09-646-028-5
US-09-543-940-9
US-09-543-940-8
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ALIGNMENTS

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Sequence 5, Application Us/09543940

Patent No. 6613742

GENERAL INFORMATION:

APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaowen
APPLICANT: Luo, Jansong
APPLICANT: Luo, Jansong
FITILE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40

CURRENT APPLICATION NUMBER: US/09/543,940

CURRENT FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,106

PRIOR APPLICATION NUMBER: 60/128,106

PRIOR APPLICATION NUMBER: 50074848

PRIOR APPLICATION NUMBER: 50074848

SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence; PEATURE:
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: peptide containing segments from N- and C-terminal; OTHER INFORMATION: regions of human SDF-1 protein US-09-543-940-5
                                                                                                                                                                                                                                                                                                 RESULT 2
US-09-543-940-4
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; LENGTH: 31
; TYPE: PRT
                                                                         GENERAL INFORMATION: Ziwei
APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaowen
APPLICANT: Zhou, Naiming
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
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Best Local (
CURRENT APPLICATION NUMBER: US/09/543,940 CURRENT FILING DATE: 2000-04-06 PRIOR APPLICATION NUMBER: 60/128,106
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Similarity 96.8%;
30; Conservative
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Pred. No. 5.2e-16;
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PRIOR FILING DATE:

1999-04-07

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GENERAL INFORMATION:

APPLICANT: Huang, Ziwei

APPLICANT: Luo, Zhaowen

APPLICANT: Luo, Zhaowen

APPLICANT: Luo, Jiansong

ITLE OF INVENTION: Chemokine-Derived Synthetic Peptides

FILE REFERENCE: 8321-40

CURRENT APPLICATION NUMBER: US/09/543,940

CURRENT FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: 60/128,106

PRIOR APPLICATION NUMBER: 60/128,106

PRIOR PILING DATE: 1999-04-07
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US-09-543-940-6
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Best Local
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LENGTH: 25
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Patent No.
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Best Local Similarity
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SOFTWARE: PatentIn V
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FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
                                                                                             APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaowen
APPLICANT: Luo, Naiming
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic
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SOFTWARE: PatentIn Ver.
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ORGANISM: Artificial Sequence
FEATURE:
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b. 6613742
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Pred. No. 2.5e-11;
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                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/181,556
FILING DATE: 14-DAN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION UMBER: 31714
REGISTRATION NUMBER: 31714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08181556 Patent No. 5525486
                                                       Matches
                                                                                       Query Match
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SEQ ID NO 7
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APPLICANT: HONJO, Tasuku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 12
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INFORMATION FOR SEQ ID NO:
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 31714
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 549-7200
TELEPHON: (703) 549-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROCESS FOR CONSTRUCTING C
TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEB; STEVENS, DAVIS, MILLER & MOSHER
STREET: 515. No. 5525486th Washington Street
CITY: Alexandria
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
LENGTH: 89 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TASHIRO, Kei APPLICANT: TADA, Hideaki
                                                                        Local
                                                                                                                                                                                                                                                              TELEPHONE: (703) 528-5313
                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                               66.9%;
1 Similarity 40.3%;
27; Conservation
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1 KPVSLSYRCPCRFFGG---
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Pred. No. 1e-08;
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Pred. No. 4.5e-10;
0; Mismatches 4
                                                     Mismatches
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D DNA CODING FOR THE
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                     -GGLKWIQE
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US-08-674-008-1
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                                                                                                                                             Sequence 1, Application US/08674008
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                              Patent No. 5756084
GENERAL INFORMATION:

APPLICANT: HONJO, Tasuku
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1' AND 1 (As I
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,084A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 2100 Pen
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 89 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 27; Conserv
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                                                                                                                                                                                                                                                           25 YLEKALN 31
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Pred. No. 1e-08;
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                      (As Amended)
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 89;
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                                                                US-09-461-912A-46
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                                                                                            SEQ ID NO 46
LENGTH: 89
TYPE: PRT
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Matches
Query Match
Best Local Similarity 40...
Matches 27; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                          APPLICANT: Damm, Deborah L.
APPLICANT: Lewicki, John A.
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: differentially expressed genes in
FILE REPERENCE: SCIOS.011A
CURRENT APPLICATION NUMBER: US/09/461,912A
CURRENT FILING DATE: 1999-12-15
                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo
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                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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FILING DATE: 1-JUL-1996
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STREET: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                66.9%;
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Score 117; DB 4; Length 89; Pred. No. 1e-08; 0; Mismatches 4; Indels
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Pred. No. 1e-08;
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   36;
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US-08-674-008-5
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Sequence 5, Application US/08674008
Patent No. 5756084
GENERAL INFORMATION:
APPLICANT: HONJO TABUKU
APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/1993
APPLICATION NUMBER: JP 280505/1993
FILING DATE: 14-OCCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7860
TELEPAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS STREET: 2100 Pennsylvania Avenue, N.W.
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CITY: Washington
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/323,084A
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20037-3202
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                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                    66.9%;
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Pred. No. 1e-08;
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Ski
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
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; ORGANISM: Mouse US-09-312-283C-421
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                          Patent No. 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                    Sequence 421, Application US/09312283C Patent No. 6573095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (202)293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
                                        LENGTH: 93
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 2805
FILING DATE: 14-CCT-1993
TELECOMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEPAX: (202)293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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STREET: 21
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TOPOLOGY: linear
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20037-3202
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Similarity 40.3%; Pred. No. 1e-08;
27; Conservative 0; Mismatches
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2100 Pennsylvania Avenue,
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; ORGANISM: Homo sapiens
US-09-919-497-95
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US-09-919-497-95
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                                                              ; OTHER INFORMATION: Description US-09-646-028-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95, App. Sequence 95, App. No. 6773883
Query Match 66.9%;
Best Local Similarity 40.3%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09646028 Patent No. 6562347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6773883 GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0 NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
                                                                                                                                                                                                                                                                      APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                             FEATURE:
                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                           ENGTH: 166
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Local Similarity 40.3%;
hes 27; Conservative
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nes 27; Conserv
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                                                                                                                                                                       FastSEQ for Windows Version 3.0
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Score 117; DB 4; I
Pred. No. 1.9e-08;
0; Mismatches 4;
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Pred. No. 1e-08;
                                                                         of artificial sequence:/note=synthetic construct
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                             Length 166;
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US-08-808-720-3
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US-09-646-028-54
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Patent No. 6562347
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                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Herrman
APPLICANT: Swanbe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN F
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEB: Genetics Insititute,
                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                     STREET: b, Cambridge
                                                                                                                                                                                                                                                                 ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 40.3%;
 FILING DATE:
CLASSIFICATION:
                                                                                                                                                        COUNTRY:
                               APPLICATION NUMBER: US/08/808,720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09646028
                                                                                                                                                                                                    87 CambridgePark
                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                              Swanberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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   530
                                                                                                                                                                                                                                                                 CHIMERIC POLYPEPTIDES
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Pred. No. 2e-08;
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                                                               Version #1.30
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ATTORNEY/AGENT INFORMATION:

NAME: Springer, Suzanne;
REGISTRATION UNBER: P-41.323
REFERENCE/DOCKET NUMBER: GI5291

TELECHOMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284

TELEPHONE: (617) 498-8284

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
US-08-808-720-3

Query Match
Best Local Similarity 40.3%; Pred. No. 3.7e-08;
MALCHES 27; Conservative 0; Mismatches 4; Indels 36; Gaps 1;
MATCHES 27; Conservative 0; Mismatches 4; Indels 24

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Db 25 YLEKALN 31

Qy 25 YLEKALN 31

Db 80 YLEKALN 86

Search completed: January 4, 2005, 15:47:50

Search completed: January 4, 2005, 15:47:50
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
Published Applications AA:*

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Gapop 10.0 , Gapext 0.5
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175
1 KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
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110.268 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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175	175	175	175	175	175	175	175	175	175	175	175	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Query Match
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Sequence 22, Appl	Sequence 21, Appl	3 5	Sequence 13, Appl	-	-	Sequence 23, Appl	-	Sequence 21, Appl	Sequence 20, Appl	-	Sequence 13, Appl	Description

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	, Appl	App1	Appl	Appl	App1	, Appl	2, Appl	App1	Appl	Appl	Appl	App1	Appl	Appl	Appl	, Appl	, Appl	Appl	Appl	, App	, App	, App	, App	, App	Appl	, Appl	, Appl	Appl	Appl	, Appl	Appl	200

ALIGNMENTS

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US-09-835-107-20
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US-09-835-107-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF
FILE REFERENCE: SMAROL2
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
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                                   Sequence 20, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Almed
APPLICANT: Arab, Lakhdar
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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SOPTWARE: PatentIn Ver. 2
SEQ ID NO 15
LENGTH: 31
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Patent No. US20020165123A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: DOMAIN
LOCATION: (15)...(18)
LOCATION: (15)...(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: Sprinesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017
NAME/KEY: MOD RES
LOCATION: (31)
LOCATION: (31)
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Local Similarity 100.0%;
hes 31; Conservative 0
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Eaves, Connie J.
Saxena, Geeta
Eaves, Connie J.
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Pred. No. 2.5e-16;
                                                                                                                                                                                                                                                                                                                                        Score 175; DB 9;
Pred. No. 2.5e-16;
; Mismatches 0;
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RESULT 4
US-09-835-107-21
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PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
                                                                                 SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. US20020165123A1
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TITLE OF IN
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                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
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TYPE: PRT

ORGANISM: Artificial Sequence

PEATURE:

PEATURE:

NAME/KEY: DOMAIN

LOCATION: (15)..(18)

OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2,

OTHER INFORMATION: or 4 glycines.
                                                                                                  SOFTWARE:
                                                                                                                      NUMBER OF SEQ ID NOS: 34
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TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
                                                                                                                                            PRIOR APPLICATION NUMBER: CA 2,335,109 PRIOR FILING DATE: 2001-02-23
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                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: SMAR012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: DOMAIN

LOCATION: (24)..(28)

COTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)

OTHER INFORMATION: residues may be joined by side chain cyclization

OTHER INFORMATION: using a lactam formation procedure.

OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SPRINGS of Laboratory:
               TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                         ENGTH:
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Eaves, Connie J.
Cashman, Johanne
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Arab, Lakhdar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 22
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22, Application US/09835107 Patent No. US20020165123A1
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                        Query Match
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-08-20 FRIOR APPLICATION NUMBER: CA 2,305,036 PRIOR FILING DATE: 2000-04-12 FRIOR APPLICATION NUMBER: US 60/232,425 PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: SMARO12
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                       NAME/KEY: DOMAIN
LOCATION: (24)..(28)
COTHER INFORMATION: Cyclized, for example (B) and lysine (K) residues
OTHER INFORMATION: may be joined by side chain cyclization using a
OTHER INFORMATION: lactam formation procedure.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-E24/K28-cyclic
OTHER INFORMATION: amide: or CTCE0022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN

LOCATION: (20)..(24)

COTHER INFORMATION: Cyclized, for example glutamate (E) and lygine (K)

OTHER INFORMATION: residues may be joined by side chain cyclization

OTHER INFORMATION: using a lactam formation.

OTHER INFORMATION: synthesised in Laboratory:

OTHER INFORMATION: Synthesised in Laboratory:
                                                                                                                                                                                                                                                                                                                                           IOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: or 4 glycines.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: DOMAIN
                                                                                                                     NAME/KEY: MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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LOCATION: (15)..
                                                                                             OTHER INFORMATION: AMIDATION
                                                                                                                OCATION:
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Baves, Connie J.
Cashman, Johanne
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Arab, Lakhdar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clark-Lewis
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100.0%;
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Pred. No. 2.5e-16;
; Mismatches 0;
Score 175; DB 9; Pred. No. 2.5e-16;
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                      Length 31;
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US-09-835-107-26

GENERAL INFORMATION: Sequence 26,

APPLICANT: Tudan, APPLICANT: Merzon APPLICANT: Arab,

Merzouk, Ahmed Arab, Lakhdar

Christopher R.

Patent No. US20020165123A1

Application US/09835107

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SEQ ID NO 23
LENGTH: 31
TYPE: PRT
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                                                                                Matches
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                                                                                                 Query Match
Best Local
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PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMARO12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/232,425 PRIOR FILING DATE: 2000-09-14
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                                                                                                                                                                                                OTHER INFORMATION: Clyclized, for example glutamate (E) and lysine OTHER INFORMATION: (K) residues may be joined by side chain OTHER INFORMATION: cyclization using a lactam formation procedure. OTHER INFORMATION: Synthesised in Laboratory: OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic OTHER INFORMATION: amide: or CTCE0021
NAME/KEY: NOD RES
LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                                        PEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: or 4 glycines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                   OTHER INFORMATION: AMIDATION
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                     1 KPVSLSYRCPCRFFGGGGLKWIQBYLEKALN
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                                                                                                   Similarity
KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN
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Eaves, Connie J.
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                                                                             100.0%; ilarity 100.0%; Conservative 0
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                                                                                                   Score 175; DB 9;
Pred. No. 2.5e-16;
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                                                                                  Mismatches
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                                                                                                                         Length 31;
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PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENCTON
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CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR PILING DATE: 2001-02-23
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Best Local (
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SEQ ID NO 26
LENGTH: 31
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APPLICANT: Merzouk
APPLICANT: Arab, I
APPLICANT: Saxena,
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CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (15)...(18)

COTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: or 4 glyclnes.

NAME/KEY: DISULFID LOCATION: (9)...(11)

COTHER INFORMATION: cystein residues may for example be involved in OTHER INFORMATION: bridge formation
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SPT-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic acid
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TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
ORGANISM: Artificial Sequence FEATURE:
                                             TYPE: PRT
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                                                                        LENGTH: 31
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Arab, Lakhdar
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Baves, Connie J.
Cashman, Johanne
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CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR PPLICATION NUMBER: 60/232,425
PRIOR PPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-04-12
PRIOR FILING DATE: 2000-04-12
PRIOR PPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
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US-10-086-177A-13
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                                                                                                                                                                  ; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - ; OTHER INFORMATION: 3-SDF-1 (55-67) acid: or CTCE0013 US-10-086-177A-13
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                                                                            Query Match
Best Local S
Matches 31
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Best Local S
Matches 31
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APPLICANT: Merzou
APPLICANT: Saxena
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APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                             TYPE: 31
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, 2 OTHER INFORMATION: or 4 glycines.

NAME/KEY: DISULFID
LOCATION: (9)..(11)
OTHER INFORMATION: Cysteine residues may for example be invloved in OTHER INFORMATION: bridge formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: Spreading for example be invloved in OTHER INFORMATION: Synthesised in Laboratory:
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                        1 KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
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Similarity 100.0%; Pred. No. 2.5e-16;
                                                                                                     Similarity
KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN
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Eaves, Connie J.
Cashman, Johanne
Clark-Lewis, Ian
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                                                                                 Conservative
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                                                                            100.0%; Score 175, DB 14;
100.0%; Pred. No. 2.5e-16;
tive 0, Mismatches 0;
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                                                                                 Gaps
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RESULT 10 US-10-086-177A-15 ; Sequence 15, Application US/10086177A

Section 1945.

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CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR PELLING DATE: 2001-04-12
PRIOR FILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR PILING DATE: 2001-02-23
NUMBER FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/855,107
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
                                                                                                                                NUMBER OF SEQ I
SOFTWARE: FastS
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 20, Application US/10086177A Publication No. US20030148940A1
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LENGTH: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tudan,
APPLICANT: Merzou
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SOFTWARE: FastSEQ for
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TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tudan, APPLICANT: Merzo
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ORGANISM: Artificial Sequence
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Eaves, Connie J.
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Baves, Connie J.
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Pred. No. 2.5e-16;
D: Mismatches 0;
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; OTHER INFORMATION: Synthesized in Laboratory: SDF-1; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-cyclic US-10-086-177A-20
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; OTHER INFORMATION: Synthesized in Laboratory: SDF-1
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic
US-10-086-177A-21

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US-10-086-177A-21
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CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR PPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                          Sequence 22, Application US/10086177A Publication No. US20030148940A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 175; DB 14; Best Local Similarity 100.0%; Pred. No. 2.5e-16; Matches 31; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%;
                                                                                                                                                  APPLICANT: Tudan,
APPLICANT: Merzo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Tudan, Christopher R. APPLICANT: Merzouk, Ahmed
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TITLE OF INVENTION: CXCR Agonist Treatment
TITLE OF INVENTION: Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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T: Salari, Hassan
INVENTION: CXCR Agonist
INVENTION: Cells
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                                                                                                                                               Merzouk, Ahmed
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Baves, Connie J.
Cashman, Johanne
                                                              Clark-Lewis, Ian
                                                                                                       Saxena, Geeta
Eaves, Connie J.
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Pred. No. 2.5e-16;
Mismatches 0;
                        Treatment
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REFERENCE: SMAR-012CIP

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; PEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) - (G)
; OTHER INFORMATION: 4-SDF-1 (55-67) - K20/E24-cyclic acid: or CTCE0021
US-10-086-177A-23
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CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR PILING DATE: 2001-04-12
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
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Best Local S
Matches 31
                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23 LENGTH: 31
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LENGTH: 31
                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OP INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OP INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tudan, Christopher R. APPLICANT: Merzouk, Ahmed APPLICANT: Saxena, Geeta APPLICANT: Eaves, Connie J.
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
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Eaves, Connie J.
Cashman, Johanne
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                                                                                          100.0%; Score 175; DB 14; 100.0%; Pred. No. 2.5e-16;
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                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Tudan, Ch
APPLICANT: Merzouk,
APPLICANT: Saxena,
APPLICANT: Eaves, C
APPLICANT: Cashman,
                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
LENGTH: 31
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Appropriate Publication No.
                                                                                   Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Clark-Lewis, Ian
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                     ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) -
OTHER INFORMATION: 4-SDF-1 (55-67) - C9/C11-cyclic acid
                                                                                   y Match 100.0%; Score 175; DB 14;
Local Similarity 100.0%; Pred. No. 2.5e-16;
nee 31; Conservative 0; Mismatches 0;
                         1 KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN
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Eaves, Connie J
Cashman, Johanne
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Saxena, Geeta
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No. US20030148940A1
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Search completed: January 4, 2005, 16:05:00 Job time : 102.131 secs

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Gapop 10.0 ,
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175
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Maximum Match 100%
Listing first 45 summaries
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Result No.

Minimum Maximum

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S73466	T45165	T22235	D96753	T22644	T35827	T40685	S01825	S30901	I50481	H96986	E72298	S06434	F82159	S45131	S30958
probable DNA prima	succinate dehydrog	hypothetical prote	Similar to disease	hypothetical prote	probable membrane	phosphatidylcholin	transforming growt	isopenicillin N ep	synapse protein SN	endo-1,4-beta gluc	hypothetical prote	homeotic protein 1	transporter, AcrB/	probable membrane	gene 13 protein -

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pre-B-cell growth-stimulating factor precursor - mouse C;Species: Mus musculus (house mouse) C;Decies: Mus musculus (house mouse) C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004 C;Accession: A53497; I59582 R;Nagasawa, T.; Kikutani, H.; Kishimoto, T. Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994 A;Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor. A;Reference number: A53497; MUID:94181581; PMID:8134392 A;Accession: A53497; MUID:94181581; PMID:8134392
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R;Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.

Exp. Cell Res. 215, 284-293, 1994

A;Title: Molecular cloning of TPARI, a gene whose expression is repressed by the tumor

A;Reference number: I53416; MUID:95073497; PMID:7982471

A;Accession: I53416
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-89 «NAG»
A;Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BAA04648.1; PID:g46845
A;Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BAA04648.1; PID:g46845
A;Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BAA04648.1; PID:g46845
A;Cross-reference NAG, Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T.
Science 261, 600-603, 1993
A;Title: Signal sequence trap: a Cloning strategy for secreted proteins and type I memb
A;Reference number: I59582; MUID:93342488; PMID:8342023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: TPAR1 C; Superfamily: beta-thromboglobulin
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C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
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A; Residues: 1-89 < RES>
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Best Local Similarity
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Pred. No. 5.4e-09;
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cytokine SDF-1-beta -
C;Species: Homo sapie
C;Date: 21-Dec-1996 #
C;Accession: G01540
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C;Superfamil
C;Keywords:
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A;Molecule type: mENA
A;Residues: 1-89 <RES>
A;Cross -references: GB:L12029;
C;Genetics:
                                                                                                                                      A;Status: preliminary;
A;Molecule type: mRNA
                                                                                                                                                                    Science 261, 600-603, 1993
A;Title: Signal sequence t:
A;Reference number: I59582
A;Accession: I81182
                                                                                                                                                                                                                                               cytokine - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revisio
C;Accession: I81182
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submitted to the EMBL Data Library,
A;Reference number: G07697
A;Accession: G01540
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A; Residues: 1-93 <SPO>
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Superfamily: beta-thromboglobulin
                                                             Superfamily:
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Best Local
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27; Conser
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66.9%;
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                                                                                                        UNIPROT:P40224; GB:L12030; NID:g393181; PIDN:AAA40101.1; PID:g393182
                                                                                                                                                                                                                                                          #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                   trap: a cloning strategy for secreted proteins 32; MUID:93342488; PMID:8342023
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Score 117; DB 2;
Pred. No. 5.7e-09;
0; Mismatches 4
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Pred. No. 5.4e-09;
0; Mismatches 4
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.7e-09;
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Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant
A;Title: Sequence and analysis of chromosome 2 of the plant
A;Title: Sequence and analysis of chromosome 2 of the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: H84604
C;Accession: H84604
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, euss, D.; Nierman, etc., Euss, Eus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
H84604
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C; Keywords: cell
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A;Residues: 1-1084 «BEV»
A;Residues: 1-1084 «DNA
A;Residues: 1-1084 «DNA
A;Residues: UNIPROT:048947; EMBL:AL050351; GSPDB:GN00062; ATSP:T22F8.250
A;Experimental source: cultivar Columbia; BAC clone T22F8
R;Arioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wittke, W.; Herth, W.; Camilleri Science 279, 717-720, 1998
Science 279, 717-720, 1998
A;Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A;Reference number: Z13745; MUID:98111412; PMID:9445479
A;Accession: T09014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                       A; Map position:
                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-1088 <STO>
A;Cross-references: UNIF
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A;Status: preliminary
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A; Accession: T08583
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                                                                                                               Genetics:
At2g21770
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RESIDUES: 1-1084 ARIS
CROSS-references: EMBLAF027173; NID:g2827140; PIDN:AAC39335.1; PID:g2827141
Ryperimental source: cultivar Columbia
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Best Local
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cell wall synthesis;
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10; Conservative
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34.9%;
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s; glycosyltransferase; hexosyltransferase
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Pred. No. 2.
                                                                                                                                                                                                                                          GB:AE002093; NID:g4417271; PIDN:AAD20396.1;
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2.8;
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Query Match

Best Local Similarity

Score Pred.

No. 2.8;

2

Length 1088;

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RESULT 9
T52028
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunist A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Status: preliminary
cellulose synthase [imported] - Arabidopsis thaliana (fragment) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P93155; EMBL:U58283; NID:g1706955; PIDN:AAB37766.1; PID:g170
A;Experimental source: strain Acala SJ-2; fiber
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C;Species: Pseudomonas aeruginosa
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A;Title: Higher plants contain homologs of the bacterial celA genes encodin A;Reference number: Z17152; MUID:97057296; PMID:8901635
A;Accession: T10797
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A; Residues: 1-469 < STO>
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A;Molecule type: mRNA
A;Residues: 1-974 <PEA>
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                 Experimental source:
                                                                                                                                                                                                                                                                                                                                                   ;Cross-references: UNIPROT:Q91168; GB:AE004668; GB:AE004091; NID:g9948446; PIDN:AAG058
;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description: involved in the synthesis of cellulose; Reywords: glycosyltransferase; hexosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                     PVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
                                                                                                                                                 PYPYDYRCPFGLGGEAGVKANLHYLENLLN 228
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pred. No. 3;
3; Mismatches
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  #text_change 09-Jul-2004
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K.; Lim,
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R;Joshi, C. submitted to the EMBL Data Library, May 1998 submitted to the EMBL Data Library, May 1998 A;Reference number: Z25890 A;Accession: T52028 A;Accession: T52028 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-1081 <JOS>
                                                                                                                                                                                                                      C;Accession: T52311
R;Kovacevic, S.; Tobin, M.B.; Miller, J.R.
R. Bacteriol. 172, 3952-3958, 1990
J. Bacteriol. 172, 3952-3958, 1990
A;Tille: The beta-lactam biosynthetis genes for isopenicillin N
A;Reference number: Z26033; MUID:90299822; PMID:1694525
A;Accession: T52311
                                                                                                                                                                                                                                                                                                                                      isopenicillin N epimerase [validated] - Streptomyces clavuligerus
C;Species: Streptomyces clavuligerus
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: SNA A;Residues: 1-233 <SAU> A;Cross-references: UNIPROT:086804; EMBL:AL031317; A;Experimental source: strain A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Datc: 05-Nov-1999 #text_change 09
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                                                                                                                             A;Cross-references: UNIPROT:P18549;
C;Genetics:
                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-398 <KOV>
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Best Local S
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RCPCRFFGGGGLKWI 22
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                                   Score 54; DB
Pred. No. 10;
2; Mismatches
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Pred. No. 3.3;
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Pred. No. 7.2;
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                                                                                                                                                 EMBL: M32324; PIDN: AAA26714.
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RIPCDFYAGSGHKWL

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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: C64104; JC5879
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, F.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: C64104
A;Accession: C64104
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                                                                                                                                                                                                   C; Function:
A; Pathway: siderophore biosynthesis
C; Superfamily: beta-alanine-pyruvate transaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data
A;Description: Cloning and
A;Reference number: Z24097
A;Accession: T46814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-aminobutyrate aminotransferase (EC 2.6.1.-) rhbA [imported] - Rhizobium C_iSpecies: Rhizobium meliloti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: beta-alanine-pyruvate transaminase C;Keywords: aminotransferase; phosphoprotein; pyri F;287/Binding site: pyridoxal phosphate (Lys) (cov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:U32776; NID:g1573969; PIDN:AAC22610.1; PID:g1573974 C;Comment: This enzyme is involved in the pathway of 1,3-diaminopropane sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-aminobutyrate aminotransferase (EC C/Species: Harmorbillo 1-57:
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101. Pharm. Bull. 21, 170-173, 1998
101. Therm. Bull. 21, 170-173, 1998
.Title: Two genes involved in the 1,3-diaminopropane production .Reference number: JC5879; MUID:98173550; PMID:9514614
.Accession: JC5879
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PVSLSYRCPCRFFGGGG----LKWIQEYLEKAL 30
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                                                                                  Conservative
                                                                                                        30.3%;
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Pred. No. 16;
3; Mismatches
                                                                                Score 53; DB 2; Length 470;
Pred. No. 16;
2; Mismatches 10; Indels
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(covalent) #status predicted
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A;Status: preliminary
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A;Residues: 1-470 <KUR>
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A;Costeric C. 1, PID.
A;Costeric C. 1, PID.
A; Costeric C. 1, PID.
A;Authors: Kahn, D.; Coste, A; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F., L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
AI3489
                                                             A;Map position: I
C;Superfamily: membrane-bound c-type cytochrome; cytochrome c homology
C;Superfamily: membrane-bound c-type cytochrome; cytochrome c homology
C;Keywords: chromoprotein; heme; iron; metalloprotein
E;84,87/Binding site: heme (Cys) (covalent) #status predicted
F;88/Binding site: heme iron (His) (axial ligand) #status predicted
F;153/Binding site: heme iron (Met) (axial ligand) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: AI3489
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows, Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilot A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytochrome c-552 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Mar-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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C; Keywords: aminotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: plasmid C;Superfamily: beta-alanine-pyruvate transaminase
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B9541F
B9541F
G:Species: Sinorhizobium meliloti
C:Species: Sinorhizobium meliloti
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                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE008917; PIDN:AAL53084.1; A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-202 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genome sequence of the facul A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: rhbA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Contents: annotation
                                                                                                                                                                                                                                                                                         A;Gene: BMEI1903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: AI3489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVSLSYRCPCRFFGGGG---LKWIQEYLEKAL 30
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28.6%;
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Pred. No. 16;
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Ivanova, Letes

Matches Local

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Perfect score:
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Maximum DB
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
                                                                                   seq length: 0
seq length: 2000000000
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Gapop 10.0 , Gapext 0.5
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175
     KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 31
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Copyright (c) 1993 - 2005 Compugen Ltd.
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QBYPD
BAA28601
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SDF1_FELCA
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QBCXM4
   AAR9102
AAR91695
Q6T7B9
AAR91696
Q9QZD1
Q80YVB
Q80YVB
Q80VYB
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Q80zw4 mus musculu Q617C0 gallus galla gallus gallu
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Q9h554 homo sapien
O62657 felis silve
P48061 homo sapien
O6ekw4 sus scrofa
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Cac10203 homo sapi
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57	57	57	57	57	57	57.5	58	58	58	58	58.	58	58
32.6	32.6	32.6	32.6	32.6	32.6	32.9	33.1	33.1	33.1	33.1	33.1	33.1	33.1
424	199	199	199	192	192	939	1087	1087	1084	1081	1069	469	460
N	N	N	N	N	N	N	N	N	N	N	N	N	N
Q9VCS4	Q8FKT6	Q83JQ0	Q7C009	CAE85184	Q707H1	Q943H3	AAP40636	Q6XZC2	Q9FGF9	065338	Q9FIB9	Q9I168	Q6D4Z7
Q9vcs4 drosophila	Q8fkt6 escherichia	Q83jq0 shigella fl	Q7c009 shigella fl	Cae85184 escherich	Q707h1 escherichia	Q943h3 oryza sativ	Aap40636 populus t	Q6xzc2 populus tre	Q9fgf9 arabidopsis	065338 arabidopsis	Q9fib9 arabidopsis	Q9i168 pseudomonas	Q6d4z7 erwinia car

ALIGNMENTS

	RE SEQUENCE F RY MEDLINE=95 RA Jiang W., RA Jiang W., RT "Molecular RT the tumor RT Exp. Cell RN [4] RN [4] RD SEQUENCE F RC STRAINAKR RA Nomura M., RL Submitted			Ξ'
OM N.A. (ISOFO L/6J; TISSUE=K \$4683; PubMed= Furuno M., Ka Ogato N., Sai Ogato N., Haseg Maxu Y., Haseg R., Hill D.P., , Kanapin A., Bradt D., Bru ragani T.A., F	ROM N.A. PubMed=799 Zhou P., Kahn S.M. Choning of TPAR1, promoter 12-0-tetr promoter 12-0-tetr Res. 215:284-293 () ROM N.A. //; Nakata Y., Uzawa (DEC-1994) to the	factor."; factor."; Proc. Natl. Acad. Sci. U.S.A. 91:2305-2309 [2] SEQUENCE FROM N.A. MEDLINE=93342488; PubMed=8342023; Tashiro K., Tada H., Heilker R., Shirozu N "Signal sequence trap: a cloning strategy type I membrane proteins."; Science 261:600-603(1993).	(TLSP). (IL); Synonyms=Sdf1; ulus (Mouse). a; Metazoa; Chordata; ; Butheria; Rodentia; ; D=10090; FROM N.A. FROM N.A. T., Kikutani H., Kish ar cloning and structu	MOUSE STANDARD; PRT; 89 AA. SDP1 MOUSE STANDARD; PRT; 89 AA. P40224; Created) 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-CT-2004 (Rel. 45, Last annotation update) Stromal cell-derived factor 1 precursor (SDF-1) Stromal tell-derived factor 1 precursor (SDF-1) cell-derived factor) (PBSF) (12-O-tetrade acetate repressed protein 1) (TPAR1) (Thymic ly
OFORM ALPHA). E=Kidney; E=Kidney; Kasukawa T., Adachi J., Bono H., Kondo S., Kasukawa T., Adachi J., Bono H., Kiyosawa H., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Segawa Y., Nogami A., Schonbach C., Gojobori T., Begawa Y., Nogami A., Quackenbush J., P., Bult C., Hume D.A., Quackenbush J., A., Matsuda H., Batalov S., Beisel K.W., Brusic V., Chothia C., Corbani L.E., Cousins S., Fletcher C.F., Forrest A., Frazer K.S., Idi M., Gissi C., Godzik A., Gough J.,	2471; 22471; 227 Tomita N., Johnson M.D., Weinstein I.B. 238 a gene whose expression is repressed by radecanoylphorbol 13-acetate (TPA)."; 2994). 248 A., Nose M., Akashi M., Suzuki G.; 259 EMBL/GenBank/DDBJ databases.	05-2309(1994) 05-2309(1994) irozu M., Naka rategy for sec	ata; Vertebrata; Eutele ognathi; Muridae; Murin T.;	MOUSE STANDARD; PRT; 89 AA. SDP1 MOUSE STANDARD; PRT; 89 AA. P40224; 01-FEB-1995 (Rel. 31, Created) 01-FEB-1995 (Rel. 31, Last sequence update) 01-CT-2004 (Rel. 45, Last annotation update) Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell Stromal timulating factor) (PBSF) (12-O-tetradecanoylphorbol 13- growth stimulating factor) (PBSF) (12-D-tetradecanoylphorbol 13- acetate repressed protein 1) (TPAR1) (Thymic lymphoma cell stimulating

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RP SEQUENCE FROM N.A. (ISOFORM ALPHA).

RC STRAIN=C57BL/60; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MELECHAIN COLLING F.S., Wagner L.H., Schemmen C.M., Schuler G.D., Hsieh F.,

RX MILLECHAIN S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX MEDLINE=2388257; PubMed=1248 M.S., Rubin G.M., Hong L.,

RX MEDLINE=2388257; PubMed=1248 M.S., Rubin G.M., Hong L.,

RX MILLECHAIN S.F., Jordan H., Max S.I., Wang J., Holgh F.S.,

RX Richards S., McZewan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

RX Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Millalon D.K., Mozny D.M., Sodergren E.J., Muzra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
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RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Magsshima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Sectou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Ahra A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Panalysis of the mouse transcriptome based on functional annotation of Co., 100 (101) (2012).
                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: Chemoattractant active on T-lymphocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Stimulates the proliferation of bone marrow-derived progenitor cells in the presence of IL-7 as well as growth of stromal cell-dependent B-cell clone DW34 cells. SUBCELULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Belongs family.
; D21072; BAA04648.1; -.; L12039; AAA40100.1; -.; L12039; AAA40101.1; -.; L12030; AAA40101.1; -.; S74318; AAB32650.1; -.; D43804; BAA07862.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P40224-2; Sequence=VSP_001057;
MILARITY: Belongs to the intercrine alpha (chemokine CxC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P40224-1;
                                                                                                                                                                                                                                                                                s requires a license agreement (S
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ,000 full-length human
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SORRER REPRESENTATION OF THE PROPERTY OF THE P
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Q8HYP0
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Best Local S
Matches 27
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8HYPO;
                                                                                                                                                                                                             HSSP;
GO; G
GO; G
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=22123042; PubMed=12126650;

MEDLINE=22123042; PubMed=12126650;

Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;

Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;

"Molecular cloning and sequencing of 25 different rhesus macaque chemokine cDNAs reveals evolutionary conservation among C, CC, CX AND CX3C families of chemokines.";

AND CX3C families of chemokines.";

Cytokine 18140-148(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:103556; Cxc112.

GO; GO:0008009; F:chemokine activity; IDA.
GO; GO:0007420; P:brain development; IDA.
GO; GO:0030334; P:regulation of cell migration;
GO; GO:0042098; P:T-cell proliferation; IMP.
InterPro; IPR0012473; C-X-C/Interlkn 8.
InterPro; IPR0012473; C-X-C/Interlkn 8.
InterPro; IPR0010473; C-X-C/Interlkn 8.
InterPro; IPR0010473; C-X-C/Interlkn 8.
InterPro; IPR00109; CXC_chmkine_smll.
Pfam; PF00048; IL8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0436; INTERLEUKINB.

PROSITE; PS00471; SMALL CYTOKHES_CXC; FALSE NEG.

Alternative splicing; Chemotaxis; Cytokine; Growth factor; Signal.

SIGNAL 1 21 Potential.

CHAIN 28 Stromal cell-derived factor 1.

DISULPID 30 55 By similarity.

DISULPID 32 71 By similarity.

VARSPLIC 89 89 K. -> KRLKM (in isoform Beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                           EMBL; AF449283; AAN76086.1; -.
HSSP; P48061; 1SDP.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008955; P:immune response; IEA.
InterPro; IPR002473; C-X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_IIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae, Macaca.
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01-JUN-2003
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BC006640;
                                                                                                                                PF00048; IL8; 1
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                                                                                               PR00436;
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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AAH06640.1;
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Pred. No. 6e-09;
0; Mismatches
Score 117;
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C4B8AD69078E55FA
                                                   AD531633C6DC2B07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
DB 2;
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Length 89;
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                                                                                                                                                                                                                                                                                                        CAC10203;
02-MAR-2004
02-MAR-2004
02-MAR-2004
BA20J15.1.1
                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=thymus;
Nishimura Y., Miyazawa T., I
Sato E., Kohmoto M., Mikami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2004
02-MAR-2004
                                                                                                   Bird
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    SEQUENCE
                                                                        Submitted
                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CAC10203
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                             NON TER
                                                 EMBL; AL137026;
                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                       Fragment).
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                                                 2000) to the CAC10203.1;
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    ME.
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ui T.;
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erived factor 1, isofo
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); Mismatches
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STROMAL CELL-DERIVED FACTOR-1A.
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                                                                                                                                                                                             Craniata; V
Catarrhini;
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    62B44E8D209C3A14 CRC64;
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RETERENT REAL REPORT OF THE PROPERTY OF THE PR
             Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yashamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muzamatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=2049374; PubMed=11042159;
                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Parthenogenote; MBDLINE=20530913; PubMed=11076861;
                                                                                                                                                                                                                                                                                                                                                               Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shiba
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected
prepare full-length cDNA libraries for rapid discovery
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Parthenogenote; MEDLINE=99279253; PubMed=10349636;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Analysis of the mouse transcriptome 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote.
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "High-efficiency
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APR-2004 (TrEMBLrel. 27, Last sequence update)
APR-2004 (TrEMBLrel. 27, Last annotation update)
APR-2004 (TrEMBLrel. 27, Last annotation update)
days embryo parthenogenote cDNA, RIKEN full-length
rary, clone:B13003ZA21 product:stromal cell derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN Genome Exploration Research Group alysis of the mouse transcriptome based c
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27; Conservative
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ency full-length cDNA cloning.";
l. 303:19-44(1999).
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                                                                                                                                                                                                                                                                                                                      N.A.
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; PubMed=11217851;
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Rodentia;
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Pred. No. (
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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Ra Salato R., Salatoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Salato R., Salatoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Ra Togawa A., Takahashi F., Takaku A., Shiraki T., Sogabe Y., Tanaka T.,
RA Togawa A., Takahashi F., Takaku A., Shiraki M., Hayashizaki Y.;
REMBL; AK045092; BAG32216.1; -.
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Best I
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SEQUENCE PROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
STRAINE=99279253; PubMed=10349636;
Carninci P., Haysshizaki Y.;
"High-efficiency full-length cDNA cloning.";
Marh..Enzymol. 303:19-44(1999).
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SEQUENCE
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last samotation update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610039H13 product:stromal cell derived factor 1, full insert
         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=C57BL/6J; T
                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based of 0,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Mammalia; Eutheria;
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STRAIN=C57BL/6J; TISSUE-Parthenogenote;
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                                                                                                                                                                              "Functional annotation of a full-length Nature 409:685-690(2001).
                                                                                                                                                                                                      RIKEN FANTOM Consortium;
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Pred. No. 6e-09;
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Sciurognathi; Muridae;
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Sano H.,
Tagami
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RESULT 7
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Matches 27
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C STRAIN-C57BL/61/ TISSUE-Kidney;

C STRAIN-C57BL/61/ TISSUE-Kidney;

A Adachi J., Alzawa K., Akahira S., Akimura T., Aono H., Arai A.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayateu N., Hirawoto K., Hirawa T., Kato H.,

A Hanagaki T., Hara A., Hayateu N., Hirawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Okazaki Y., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi R., Tanaka T.,

Tejima Y., Toya T., Yamanura T., Yamanaka I., Yasunishi A.,

Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.,

Submitted (Apr.-2002) to the EMBL/GenBank/DDBJ databases.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                               CAG29279;
20-MAY-2004
20-MAY-2004
20-MAY-2004
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MEDINE-2053013) PubMed-11076661;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sagaki N., Carninci P.,
Shibata K., Itoh M., Aizawa K., Natsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
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Mammalia; Eutheria;
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Gateway(TM)
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Hori F.,
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RESULT 8
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Best Local S
Matches 27
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Matches :
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SEQUENCE
                                                              SDP1_PELCA STANDARD; PRT; 93 AA. 062657; PRC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Stromal cell-derived factor 1 precursor (SDF-1)
Name=CXCL12; Synonyms=SDP1;
                                                                                                                                                                                                                                           PBLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2000) to the EMBL; AL137026; CAC10202.1; HSSP; P48061; ISDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:000809; F:chemokine activity;
GO; GO:0006955; P:immune response; IEA
InterPro; IPR002473; C-X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ol.MAR-2001 (TrEMBLrel. 16, Created)
Ol.MAR-2001 (TrEMBLrel. 16, Last sequence update)
Ol.WIN-2003 (TrEMBLrel. 24, Last sequence update)
BA20J15.1.2 (Stromal cell-derived factor 1, isoform beta)
TISSUE=Thymus;
MEDLINE=98450506;
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0436; INTE
SMART; SM00199; SCY;
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                                                             NCBI_TaxID=9685;
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27; Conserv
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 PubMed=9777331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10510 MW;
                              (ISOFORMS ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 117; DB Pred. No. 6.2e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 6e-09;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEF0C402B44E8D20 CRC64;
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                                                                                                                                            (CXCL12)
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                                                                               Euteleostomi; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          36;
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SDF1_HUMAN
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Best Local (
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                                                                                                                                                          SDF1 HUMAN
P48061;
01-FEB-1996
01-FEB-1996
01-OCT-2004
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-!- FUNC
                                                                                         01-PBB-1996 (Rel. 33, Created)
01-PBB-1996 (Rel. 33, Last sequence update)
01-CCT-2004 (Rel. 45, Last annotation update)
Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (hIRH) [Contains: SDF-1-beta(3-72); SDF-1-alpha(3-67)].
SDF-1-alpha(3-67);
Name=CXCL12; Synonyms=SDF1;
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DISULFID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB011966; BAA28602.1; -.
HSSP; P48061; 1SDF.
InterPro; IPR002473; C-X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_IL8.
InterPro; IPR001089; CXC_chmkine_smll.
Pfam; PF00048; IL8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION:
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cai J.S., Sato E., Kohmoto M., Mil
"Molecular cloning and sequencing
factor-1 alpha and beta.";
                                             Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
 SEQUENCE FROM N.A
                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . J. Immunogenet. 25:303-305(1998). FUNCTION: Chemoattractant active o not neutrophils.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity 27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                YLEKALN
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                                                                                                                                                                                                                            STANDARD;
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ing; Chemotaxis; Cytokine; Growth factor; Signal.
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                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.9%;
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By similarity.
By similarity.
Missing (in isoform Alpha).
/FTId=VSP 001055.
/#4FC7637IIE9BE37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 117; DB 1;
Pred. No. 6.3e-09
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                                               Craniata; V
Catarrhini;
                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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feline
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                                                 Vertebrata;
i; Hominidae;
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Length 93; Indels

36;

-GGLKWIQE Gaps

81 24

Euteleostomi;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                         splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ikeda Y., Izumiya Y., Nakamura
M., Mikami T.;
                                                                                                                                                                                                                                                the intercrine alpha (chemokine CxC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on T-lymphocytes,
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         stromal cell-derived
                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      monocytes,
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., RA Klauener R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D., RA Altgchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glabbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Tand mouse cDNA sequences.";

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Deloukas P., Barthrowl M.E., Grafham D.V., Rubenfield M., French L., Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K., Hunt S.E., Andrews T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L., Taylor A., Battles J., Bird C.P., Ainscough R., Almeida J.P., Taylor A., Battles J., Bird C.P., Ainscough R., Baggley C.L., Bailey J., Babbage A.K., Baggley C.L., Bailey J.
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SEQUENCE FROM N.A.
MEDLINE=96039262; PubMed=7490086;
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Nakano T., Inazawa J., Tashiro
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28:495-500(1995)
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SDF-1ALPHA (3-67) AND SDF-1BETA (3-72)
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reduced chemoattractant active on T-lymphocytes, monocytes, but not neutrophils. SDF-1-beta(3-72) and SDF-1-alpha(3-67) show a reduced chemotactic activity. Binding to cell surface proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) and thus to preserve activity on local sites.

-!- SUBCELLULAR LOCATION: Secreted.
-!- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=Beta; Synonyms=SDF-1-beta(1-72);

IsoId=P48061-1; Sequence=Displayed;

Name=Alpha; Synonyms=SDF-1-alpha(1-68);

IsoId=P48061-2; Sequence=VSP 001056;

PTM: Processed forms SDF-1beta(3-72) and SDF-1alpha(3-67) are produced after secretion by proteolytic cleavage of isoforms Beta and Alpha, respectively. The N-terminal processing is probably achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus. The C-terminal processing of isoform Alpha is reduced by binding to heparin and, probably, cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coreceptor.";
proc. Natl. Acad. Sci. U.S.A.
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PubMed=1425775; DOI-10.1182/blood-2003-08-2857;
De La Luz Sierra M., Yang F., Narazaki M., Salvucci O., Davis D.,
Yarchoan R., Zhang H.H., Fales H., Tosato G.;
"Differential processing of stromal-derived factor-lalpha and beta
explains functional diversity.";
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Crump M.P., Gong J.H., Loetscher P., Ra
Arenzana-Seisdedos F., Virelizier J.L.,
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SIMILARITY: Be
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EMBL; U16752; AAA97434.1; -.
EMBL; L136033; AAB39333.1; -.
EMBL; L136034; AAB39333.1; -.
EMBL; L136034; AAB39333.1; -.
EMBL; U19495; AAB40516.1; -.
EMBL; AL137026; CAC10203.1; -.
EMBL; BC039893; AAH39893.1; -.
EMBL; BC039893; AAB39893.1; -.
EMBL; BC039893; AAB39833.1; -.
EMBL; BC039893; AAB39333.1; -.
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EMBL; BC03983; AAB39333, AAB3933; EMBJ9333, AAB3933; EMBJ9333, AAB3933, AA MIM; 600835; GO; GO:000800 GO; GO:000510 GO; GO:000687 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restue by non-profit institutions as long as its content modified and this statement is not removed. Usage by an or send an email to license@isb-sib.ch). entities ; GO:0008009; ; GO:0005102; ; GO:0006874; requires a license agreement F:chemokine activity; TAS. F:receptor binding; TAS. P:calcium ion homeostasis; TAS (See http://www.isb-sib restrictions and EMBL a collaboration for .ch/announce, outstation in no way ဓ္ဌ

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PubMed=15242943;

Ledger T.N., Pinton P., Bourges D., Roumi P.,

"Development of a macroarray to specifically
gene expression in Swine.";
Clin. Diagn. Lab. Immunol. 11:691-698 (2004).

EMBL; AY312066; AAAQ84094.1; -.

SEQUENCE 116 AA; 12622 MW; 2A1BCE0551C2BI
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Mammalia; Eutheria;
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PROSITE; PS00471; SMALL_CYTOKI
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InterPro; IPR001811; Chemokine_IL8.
InterPro; IPR001089; CXC_chmkine_smil.
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                                                                                                                                                                                                                    Sus scrofa (Pig).
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GO:0006935; P:chemotaxis; TAS.
GO:0008015; P:chemotaxis; TAS.
GO:0007186; P:cprotein coupled receptor protein signalin.
GO:0006955; P:lmmune response; TAS.
GO:0008064; P:regulation of actin polymerization and/or d.
GO:0009615; P:response to virus; TAS.
GO:0007165; P:signal transduction; TAS.
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Cetartiodactyla; Suina; Suidae;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 6.3e
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 117; DB 1;
Pred. No. 6.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missing (in isoform Alpha) /FTId=VSP_001056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stromal cell-derived factor 1. SDF-lbeta(3-72). SDF-lalpha(3-67).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    505B5A29C2B44E8D CRC64;
   2A1BCE0551C2BEAB
                                                                      D., Roumi P., specifically
                                                                                                                                                                                                                                                                                                                                           116
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                                                                    , Salmon
analyze
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                               Euteleostomi;
Sus.
                                                                    H., Oswald I. immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GGLKWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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QROZWAT 12
QROZWATA
ID QROZWATA
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ID CAC11
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OC MAMMAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W. MEDLINE=22388257; PubMed=12477932;

X. MEDLINE=22388257; PubMed=12477932;

A. Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

X. Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A. Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A. Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A. Boate S., Loquellano N.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

A. Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A. Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

A. William M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B. Hakeney R.M., Touchman J.W., Green R.D., Dickson M.C.,

B. Blakelev R.W., Touchman J.W., Green R.D., Dickson M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003
01-JUN-2003
01-MAR-2004
                                                 PRINTS; I
SMART; SN
SEQUENCE
                                                                                                                                   MGD; MGI:103556; Cxcl12.

GG; GO:0008009; F:chemokine activity; IDA.

GG; GO:0007420; P:brain development; IDA.

GG; GO:0007281; P:germ cell development; IDA.

GG; GO:0007381; P:germ cell migration; IDA.

GG; GO:0008354; P:germ cell migration; IDA.

GG; GO:003035; P:noblitive regulation of cell migration; IDA.

GG; GO:003035; P:positive regulation of cell migration; IDA.

GG; GO:0042098; P:T-cell proliferation; IMP.

InterPro; IPR002473; C-X-C/Interlkn 8.

InterPro; IPR002473; C-X-C/Interlkn 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q80ZW4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffa: Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Bul Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Generation and initial analysis of and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                         P48061; 1SDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                               BC046827; AAH46827.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
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                                                                            PR00436; INT
SM00199; SCY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 40...
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
57BL/6; TISSUB=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLEKALN
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                                                   Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
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                                                                                                       INTERLEUKINB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sci.
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Rodentia;
                                                   15529 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66.98;
  66.98;
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24,
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Last sequence update)
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Pred. No. 7.8e-09;
0; Mismatches 4
  Score 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                   04B47DAB6904DF77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            more than 15,000
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  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases.
Length 137;
                                                   CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Butterfield
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Query Match

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AARBB102
ID AARBB102
ID AARB
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Best Local
Matches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Read LR., Cumberbatch J., Sharif S.;
Submitted (OCT-2003) to the EMBL/GenB
EMBL; AY429472; AAR91695.1; -.
EMBL; AY451855; AAR891602.1; -.
EMBL; AY451855; AAR891602.1; -.
InterPro; IPR002473; C-X-C/Interlkn 8
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
PRINTS; PR00446; INTERLEUKIN8.
SMART; SM00199; SCY; 1.
SEQUENCE 89 AA; 10104 MW; 21E53D1
                                                                                                                                                                                                                                          AAR88102;
02-MAR-2004 (TrEMBLrel. 27, C
02-MAR-2004 (TrEMBLrel. 27, L
02-MAR-2004 (TrEMBLrel. 27, L
Stromal cell derived factor 1
                                                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Raz E., Stebler J.;
Submitted (OCT-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gailus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6T7C0
      SEQUENCE FROM N.A
                                                       NCBI_TaxID=9031;
                                                                                                    Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                   AAR88102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Stromal cell-derived factor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q6T7C0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
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RAZ E., Stebler J.;

"Chicken SDF-lalpha.";

Submitted (OCT-2003) to the EM
EMBL; AY429472; AAR91695.1; -.

SEQUENCE 89 AA; 10104 MW;
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Read L.R., Cumberbatch J., Sharif S.;
Read L.R., Cumberbatch J., Sharif S.;
"haracterization of Chicken SDF-1.";
"haracterization of the EMBL/GenBank/DDBJ d
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ d
EMBL; AY451855; AAR88102.1; -.
SEQUENCE 89 AA; 10104 MW; 21E53D121A557965
                                                                                                                                                                                                                                                                                                              14-APR-2004 (TrEMBLrel. 27, Created)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Stromal cell-derived factor-1 alpha.
Stromal cell-derived factor-1 alpha.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi,
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phassiani
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Pred. No. 8.4e-09;
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173.671 Million cell updates/sec
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and is derived is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	w	2	,	Result No.	
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ALIGNMENTS

CCCCXRXTTTXXRXFRRRRRRRRRRXBXRXBXAXXRXAXXBXAXXAXXAXX Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation. Synthetic. AAB47694 standard; peptide; SDF-1(1-14) - (G)3 -30-JAN-2002 Key Modified-site AAB47694; (first entry) Location/Qualifiers /note= "C-terminal amide" SDF-1(55-67) amide. 30 ₿

18-OCT-2001. WO200176615-A2

12-APR-2000; 2000CA-02305036. 14-SEP-2000; 2000US-0232425P. 23-FEB-2001; 2001CA-02335109.

12-APR-2001; 2001WO-CA000540

(UYBR-) UNIV BRITISH COLUMBIA. (CHEM-) CHEMOKINE THERAPEUTICS CORP.

Salari H, Cashman J, Merzouk A, Aral Clark-Lewis I; Arab L, Tudan CR, Saxena G, Eaves CJ;

WPI; 2002-025882/03.

CXC receptor 4 agonists that reduces hematopoietic and susceptibility to cytotoxic agents, are useful peripheral blood stem cell transplantation. cell multiplication for bone marrow or

Example 1; Page 42; 74pp; English.

The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4

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RESULT 2
AAB47692
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The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoletic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematoric cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic
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Cashman J,
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                                                                                                                                                                                                                     CXC receptor 4 agonists that reduces hematopoietic and susceptibility to cytotoxic agents, are useful peripheral blood stem cell transplantation.
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14-SEP-2000; 2000US-0232425P.
23-FEB-2001; 2001CA-02335109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologeallogenic; bone marrow; stem cell; transplantation.
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Similarity 100.0%;
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Clark-Lewis
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Pred. No. 1.5e-1
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                                                                                                                                                                                                                                                        The present sequence is a synthetic chemokine peptide of the chemokine stromal cell-derived factor-1 (SDF-1). It is useful for inhibiting the entry of Human immunodeficiency virus-1 (HIV-1) into CXC chemokine receptor 4 (CXCR4)-expressing cells and for treating HIV infection. The novel SDF-1 derived synthetic peptides have enhanced activity over separate peptides derived only from the N-terminal segment of SDF-1 or derived only from the X-terminal segment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel synthetic chemokine peptides of stromal cell derived for inhibiting HIV-1 entry and infection via CXC chemokine and in HIV infection treatment and prophylaxis.
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                                                                                                                                                                                                            Sequence
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                                                                                                    Score 158.5; DB 3;
Pred. No. 4.8e-15;
0; Mismatches 0;
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No. 1.5e-16;
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RESULT 4 AAB47693 ID AAB4

AAB47693 standard; peptide;

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14-SEP-2000;
23-PEB-2001;
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                                                                                                                                                                                                                                                                                                         is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic bone marrow or peripheral blood stem cell transplantation, or
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               SDP-1(1-14)
                                         30-JAN-2002
                                                                                            AAB47686 standard;
                                                                                                                                                                                                                                                                    Sequence 31
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                                                                                                                                                                                                                                                                                                autoimmune disease
                                                                                                                                                                                                                              ocal Similarity
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Clark-Lewis
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2000US-0232425P.
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               (G) 4 -
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                                                                                            peptide;
                                                                                                                                                                                                                           93.8%;
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               SDF-1 (56-67)
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Pred. No. 4.8e-15;
D; Mismatches (
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Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
WPI;
                                                     Salari H,
                                                                                                                                           12-APR-2000; 2000CA-02305036.
14-SEP-2000; 2000US-0232425P.
23-FEB-2001; 2001CA-02335109.
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                                    Cashman
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2002-025882/03
                                                                                     UNIV BRITISH COLUMBIA. CHEMOKINE THERAPEUTICS
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                                  Merzouk A, I
Clark-Lewis
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CXC receptor 4 agonists that reduces hematopoietic and susceptibility to cytotoxic agents, are useful peripheral blood stem cell transplantation. cell multiplication for bone marrow or

Claim 8; Page 58; 74pp; English.

The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent. The CXCR4 agonist is used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, particularly in a patient with cancer requiring autologous or alloganic bone marrow or peripheral blood stem cell transplantation, or autoimmune disease

Sequence 31 B

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                            Matches
                                    Query Match
Best Local Similarity
                           30;
KPVSLSYRCPCRFF-GGGLKWIQEYLEKALN
                            Conservative
                                   93.8%;
                          Score 158.5; DB 5;
Pred. No. 4.8e-15;
0; Mismatches 0;
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RESULT 6
AAB47706
AAB47706
peptide;
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KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN

31

SDF-1(1-14) - (G)4 -SDF-1(55-67)-C9/C11-cyclic acid.

30-JAN-2002

(first entry)

Haematopoletic cell; multiplication; CXC chemokine receptor 4; CXCR4 agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autolo allogenic; bone marrow; stem cell; transplantation.

Synthetic

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RESULT 7
AAB47702
ID AAB4
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AC AAB4
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Cashman J,
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14-SEP-2000;
23-FEB-2001;
                                                                                                                                                                                                                                        Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologallogenic; bone marrow; stem cell; transplantation.
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                                                                         Modified-site
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Clark-Lewis
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2000US-0232425P.
2001CA-02335109.
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                                                                                                Location/Qualifiers
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Modified-site

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salari F
Cashman
                                                                                       Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4 agonist; stromal cell derived factor one; SDF-1; autoAmmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autolo allogenic; bone marrow; stem cell; transplantation.
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14-SEP-2000; 2000US-0232425P.
23-FEB-2001; 2001CA-02335109.
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Clark-Lewis
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ilarity 96.8%;
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Pred. No. 4.8e-15;
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RESULT 9
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                                                                                                                             Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologiallogenic; bone marrow; stem cell; transplantation.
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14-SEP-2000; 2000US-0232425P
23-PEB-2001; 2001CA-02335109
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RESULT 10
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14-SEP-2000; 2000US-0232425P.
23-FEB-2001; 2001CA-02335109.
                                                                                                          Haematopoletic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologous; allogenic; bone marrow; stem cell; transplantation.
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               Disulfide-bond
Modified-site
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Clark-Lewis
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ilarity 96.8%;
Conservative
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                           Location/Qualifiers
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/note= "C-terminal amide"
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14-SEP-2000;
23-FEB-2001;
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Clark-Lewis
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2000US-0232425P.
2001CA-02335109.
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/note= "C-terminal amide"
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Pred. No. 4.8e-15;
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12-APR-2001; 2001WO-CA000540

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14-SEP-2000; 2000US-0232425P.
23-FEB-2001; 2001CA-02335109.
                                                                                                                                                          Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4 agonist; stromal cell derived factor one; SDF-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autolo allogenic; bone marrow; stem cell; transplantation.
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                                                                                           Modified-site
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Clark-Lewis
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                                                                                                                                                                                                                                                     (first entry)
                                                                                          Location/Qualifiers
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                                                                             "C-terminal amide"
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Pred. No. 4.8e-15;
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14-SEP-2000;
23-FEB-2001;
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Cashman J,
                                                                                                                                                                                                        Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4; agonist; stromal cell derived factor one; SDP-1; autoimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autologiallogenic; bone marrow; stem cell; transplantation.
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                                                                                                                                                                                                                                                                                                                                                            AAB47700 standard; peptide; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31
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12-APR-2000;
                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                              SDF-1(1-14) -
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                          12-APR-2001; 2001WO-CA000540.
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                                                                                                                                       Key
Modified-site
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Clark-Lewis
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2000US-0232425P.
2001CA-02335109.
2000CA-02305036
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                                                                                                                                    Location/Qualifiers 24. .28
                                                                                                                       note= "Joined by side chain cyclization using lactam/
                                                                                                            ormation"
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                                                                                                                                                                                                                                                                            SDF-1(55-67)-E24/K28-cyclic acid.
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Pred. No. 4.8e-15;
0; Mismatches 0
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Matches 30
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                                                                                                                                                                                                                               Haematopoietic cell; multiplication; CXC chemokine receptor 4; CXCR4 agonist; stromal cell derived factor one; SDF-1; autolimmune disease; macrophage inflammatory protein 1-alpha; MIP-1-alpha; cancer; autolo allogenic; bone marrow; stem cell; transplantation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CXC receptor 4 agonists that reduces hematopoietic and susceptibility to cytotoxic agents, are useful peripheral blood stem cell transplantation.
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Modified-site
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                                                                                                                                                                                                                                                                                                    SDF-1 (1-14)
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23-FEB-2001; 2001CA-02335109
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30; Conservative
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J, Clark-Lewis
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Pred. No. 4.8e
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1.8e-15;
hes 0;
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12-APR-2000; 2000CA-02305036

12-APR-2001; 2001WO-CA000540

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RESULT 15
AAB47714
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14-SEP-2000;
23-FEB-2001;
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Cashman J, Clark-Lewis
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23-FEB-2001;
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1 Similarity 96.8%;
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Merzouk A,
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2000US-0232425P.
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2001CA-02335109.
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Pred. No. 4.8e-15;
0; Mismatches 0;
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The sequences given in AAB47680-717 represent peptides which may be used in the method of the invention for reducing the rate of hematopoietic cell multiplication. These peptides act as CXC chemokine receptor 4 (CXCR4) agonists to the cells. These peptides are based on stromal cell derived factor one (SDF-1) with some also containing sequences derived from macrophage inflammatory protein 1-alpha (MIP-1-alpha). They can be used to reduce susceptibility of hematopoietic cells to a cytotoxic agent, by administering one of the agonist peptides to the cells prior to or during exposure of the cells to the cytotoxic agent, particularly in a patient with cancer requiring autologous or allogenic been marrow or peripheral blood stem cell transplantation, or
Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                              CXC receptor 4 agonists that reduces hematopoietic cell multiplication and susceptibility to cytotoxic agents, are useful for bone marrow or peripheral blood stem cell transplantation.
                                                an
                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 47; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Савhman J,
                                                autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark-Lewis
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밁 8 Matches Query Match Best Local 1 KPVSLSYRCPCRFF-GGGLKWIQEYLEKALN ch 93.8%; 1 Similarity 96.8%; 30; Conservative KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN 0; Score 158.5; DB 5 Pred. No. 4.8e-15; 0; Mismatches 0 3 30 5. 0 Length 31; Indels ۲. Сарв 1;

Search completed: January Job time : 67.9672 secs 2005, 15:46:50

Title: Perfect

Sequence:

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Sequence 2, A Sequence 4, A Sequence 7, A Sequence 7, A Sequence 285 Sequence 2620 Sequence 2620

12, Appl 6, Appli 32272, A 25662, A 16, Appl 16, Appl 16, Appli 4, Appli 4, Appli 7, Appli 7, Appli 7, Appli 8620, Ap 8620, Ap 263404, A 25, Appl

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re greater than or equal to the score of the result being put
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; Sequence 4, Application US/09543940
; Patent No. 6613742
; GENERAL INFORMATION:
; APPLICANT: Huang, Ziwei
; APPLICANT: Luo, Zhaowen
; APPLICANT: Luo, Zhaowen
; APPLICANT: Luo, Jiansong
; APPLICANT: Luo, Jiansong
; TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
; FILE REFERENCE: 8321-40
; CURRENT APPLICATION NUMBER: US/09/543,940
; CURRENT FILLING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/128,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Huang, Ziwei
APPLICANT: Luo, Zhaowen
APPLICANT: Lou, Naiming
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
TENGIH: 31
TYPE: PRI
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
; OTHER INFORMATION: peptide containing segments from N- and C-terminal;
OTHER INFORMATION: regions of human SDF-1 protein
US-09-543-940-5
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Patent No. 6613742
GENERAL INFORMATION:
Huang, Ziwei
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nilarity 96.8%;
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US-09-023-905A-3
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US-08-117-083-61
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US-09-888-586-7
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US-09-252-991A-26204
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SEQ ID NO 6
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Patent No. 5525486
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Best Local Similarity
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                 GENERAL INFORMATION:
APPLICANT: HONJO, TABUKU
APPLICANT: TASHIRO, Kei
APPLICANT: TADA, Hideaki
APPLICANT: TADA, Hideaki
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: PROCESS FOR CONSTRUCTING OT TITLE OF INVENTION: AND NOVEL POLYPEPTIDE AND NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEVENS, DAVIS, MILLER & MOSHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 8321-40
CURRENT APPLICATION NUMBER: US/09/543,940
CURRENT FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/128,106
PRIOR FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Zhou, Naiming
APPLICANT: Luo, Jiansong
TITLE OF INVENTION: Chemokine-Derived Synthetic Peptides
--- befreence: 8321-40
US/09/543,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORCANISM: Artificial Sequence
ORCANISM: Artificial Sequence
FEATURE;
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide containing segments from N- and C-terminal
OTHER INFORMATION: regions of human SDF-1 protein
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Luo, Zhaowen
Naiming
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26; Conservative
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                                                                                                                                                                                                                                                                                                                                   LSYRCPCRFFGGGLKWIQEYLEKALN 30
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                                                                                                                                                                                                                                                                                                 LSYRCPCRFF-GGLKWIQEYLEKALN 25
                                                                                                                                                                                                     Application US/08181556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09543940
STEVENS, DAVIS, MILLER & MOSHER 515 No. 5525486th Washington Street
                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-323-084A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Applic
Patent No. 5563048
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Best Local Similarity 40.3%;
Matches 27; Conservative
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TELEX: 89-2746
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
COMPUTER: PM PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
APPLICATION NUMBER: US/08/323,084A FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: JF 280505/1993 FILING DATE: 14-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 5-22098
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: POULOS III, James A.
REGISTRATION NUMBER: 31714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: SUGHRUB, MION, ZINN, MACPEAK & SEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TETELECOMMUNICATION INFORMATION: TELEPHONE: (703) 549-7200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 528-5313
                                                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20037-3202
                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/181,556
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                                                                                                                                                                                                                                                                                            2100 Pennsylvania Avenue, N.W.
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                                                                                                                               Version #1.25
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TELECOMMUNICATION INFORMATION: TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860

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GENERAL INFORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: TADA, Hideaki
APPLICANT: TADA, Hideaki
ITITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
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                                                                      ; MOLECULE TYPE: protein US-08-674-008-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-674-008-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-323-084A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202)293-7060
TELEXX: (202)293-7860
TELEXX: 6491103
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 89 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Applic
Patent No. 5756084
     Query Match 70.1%;
Best Local Similarity 40.3%;
Matches 27; Conservative
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Best Local
                                                                                                                                                          TELEX: 6491103
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                            FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7860
TELEFAX: (202)293-7860
                                                                                                                            TYPE: a
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 1-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 40.3 es 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22
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                                                                                                                        : 89 amino acids
amino acid
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                                                                                                            linear
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     Score 118.5; DB 1;
Pred. No. 2.9e-09;
0; Mismatches 3;
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Pred. No. 2.9e-09;
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                                   Length 89;
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       Indels
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   37;
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     Gaps
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APPLICANT: White, R. Tyler
APPLICANT: White, R. Tyler
APPLICANT: White, R. Tyler
APPLICANT: White, R. Tyler
APPLICANT: Damm, Deborah L.
APPLICANT: Lowicki, John A.
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TITLE OF INVENTION: Methods for detection and use of
TURERY APPLICATION NUMBER: US/09/461,912A
CURRENT FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,008
PRIOR FILING DATE: 1998-12-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-08-323-084A-5
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US-09-461-912A-46
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                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08323084A
Patent No. 5563048
GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: SHIROZU, MICHIO
APPLICANT: TADA, HIDEAKI
TITLE OF INVENTION: No. 5563048el Polypeptides and DNAs encoding them
NUMBER OF SEQUENCES: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC competible
COMPUTER: IEM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                  STREET: 2100 Penu
CITY: Washington
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                                                                                                                                                                                       RY: U.S.A.
20037-3202
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Similarity 40.3%;
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                                           US/08/323,084A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 118.5; DB 4
Pred. No. 2.9e-09;
                                                                                     Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -------GLKWIQE 23
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APPLICATION NUMBER: JP 28050 FILING DATE: 14-OCT-1993 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)293-7060

PRIOR APPLICATION DATA:

JP 280505/1993

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TELERAX: (401103
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
TYPE: amino acid
US-08-674-008-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-323-084A-5
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Patent No. 575608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,084
FILING DATE: 14-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 280505/19
FILING DATE: 14-OCT-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atent No. 3,700 GENERAL INFORMATION:
HONJO, Tasuku
                                                                             TELEX: 6491103
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/674,008
FILING DATE: 1-JUL-1996
        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHIROZU, Michio
APPLICANT: TADA, Hideaki
TITLE OF INVENTION: HUMAN STROMAL DERIVED
TITLE OF INVENTION: FACTOR 1' AND 1 (As Amended)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                    LENGTH: 93 amino acids
TYPE: amino acid
TOPOLOGY: linear
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nes 27; Conserv
                                                                                                                              TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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20037-3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08674008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                 (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUGHRUE,
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GENERAL INCORMATION:

GENERAL INCORMATION:

APPLICANT: Mutter, George L.

APPLICANT: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER

FILE REFERENCE: B001/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 100

SOFTWARE: Patentin version 3.0

SOFTWARE: Patentin version 3.0

TYPE: PRT

COGANISM: Homo sapiens

US-09-919-497-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watton, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011.2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 421
LENGTH: 93
TYPE: PRT
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US-09-312-283C-421
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Best Local S
Matches 27
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Matches
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Local Similarity
Query Match 70.1%;
Best Local Similarity 40.3%;
Matches 27; Conservative
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Patent No. 6773883
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40.3%;
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Score 118.5; DB Pred. No. 3e-09; 0; Mismatches
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Pred. No. 3e-09;
0; Mismatches
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                              Length 93;
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 37;
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GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
ITILE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKING-TUMOR ANTIGEN FUSION
FILE REFERENCE: 14014.0316/p
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER: OF SEQ ID NOS: 57
NUMBER: OF SEQ ID NOS: 57
NUMBER: OF SEQ ID NOS: 57
                                                                                                              CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR PILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 54
LENGTH: 177
TYPE: PRT
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-646-028-54
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                                                          ; FEATURE: ; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct US-09-646-028-54
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US-09-646-028-5
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US-09-646-028-5
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/09646028 Patent No. 6562347 GENERAL INFORMATION:
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SEQ ID NO 5
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Best Local (
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Patent No. 65623
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                             APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUS:
FILE REFERENCE: 14014.0316/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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70.1%;
40.3%;
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Pred. No. 5.4e-09;
Score 118.5; DB 4;
Pred. No. 5.7e-09;
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                Length 177
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; Sequence 3, Application US/09467638; Patent No. 6730296; GENERAL INFORMATION: APPLICANT: Herrmann, Steve; APPLICANT: Swanberg, Stephen
                                                                              RESULT 15
US-09-467-638-3
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US-08-808-720-3
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Patent No. 6100387
GENERAL INFORMATION:
APPLICANT: Herrmann, Steve
APPLICANT: Swanberg, Stephen
TITLE OF INVENTION: CHEMOKINE DOMAINS
TITLE OF INVENTION: CHEMOKINE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,720
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Springer, Suzanne
REGISTRATION NUMBER: P-41,323
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Insititute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 326 amino acids TYPE: amino acid
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27; Conserv
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nilarity 40.3%;
Conservative
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                                                                                                                                                                                                                                                                        Score 118.5;
Pred. No. 1.1e
0; Mismatches
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Steve Stephen

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NAME: Sprunger, Suzanne.

REGISTRATION NUMBER: P-41,323
REFERENCE/DOCKET NUMBER: GI5291
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 326 amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-467-638-3
Search completed: January 4, 2005, 15:47:49 Job time: 30.0492 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MARCHANGE STATE: MARE: MARE: MARE: MARE: MARE: MARE: MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPARISHE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/467,638
FILING DATE:
CLASSIFICATION:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOMBER: US/08/808,720
FILING DATE: NUMBER: US/08/808,720
ATTORNEY/AGENT INFORMATION:
APPLICATION STATES
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TITLE OF INVENTION: CHEMOKINE DOMAINS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetice Institute, Inc.
STREET: 87 CambridgePark
CITY: Cambridge
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                                                                                                   80 YLEKALN 86
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Minimum
Maximum
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Perfect score:
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Match
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Copyright (c) 1993 - 2005
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/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                   US-09-835-107-12
US-10-9-835-107-14
4 US-10-086-177A-14
US-10-086-177A-14
US-09-835-107-15
US-09-835-107-20
US-09-835-107-21
US-09-835-107-22
US-09-835-107-23
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US-09-835-107-27
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Compugen Ltd.
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Sequence 12, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 15, Appl
Sequence 20, Appl
Sequence 21, Appl
Sequence 22, Appl
Sequence 23, Appl
Sequence 27, Appl
                                                                                                                                                                                                                                         Description
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-09-852-424-	-09-852-424-	-09-852-424-7	US-09-852-424-95	9-	-852-424-12	US-09-852-424-75	-09-852-424-1	09-852-424-	09-852-42	09-852-424-	09-852-424-	09-852-424-	US-10-086-177A-25	10-086-177A-2	US-09-835-107-25	US-09-835-107-24	US-10-086-177A-19	US-10-086-177A-17	US-09-835-107-19	US-09-835-107-17	US-10-086-177A-18	P	US-09-835-107-18	US-09-835-107-16	-10	-10-086-177A-2	US-10-086-177A-23	US-10-086-177A-22	-10-086-177A-2	-10-086-177A-2	-10-086-177A-1
99,	94,	Sequence 79, Appl	95,	125,	e 123,	75,	e 135,	134,	133,	124,	122,	74,	e 25,	e 24, App	•	24,	Sequence 19, Appl	e 17, App	Sequence 19, Appl	•	e 18	e 16	Sequence 18, Appl	•	e 27	e 26	N	N	e 21	20	e 15,

ALIGNMENTS

Sequence 12, Application US/09835107 Patent No. US20020165123A1 GENERAL INFORMATION:

APPLICANT:

APPLICANT: APPLICANT:

Saxena, Geeta Eaves, Connie J. Merzouk, Ahmed Arab, Lakhdar

APPLICANT: Tudan,

Christopher R.

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CURRENT FILING DATE: 2001-08-20

FRIOR APPLICATION NUMBER: CA 2,305,036

PRIOR APPLICATION NUMBER: CA 2,305,036

PRIOR APPLICATION NUMBER: US 60/232,425

PRIOR APPLICATION NUMBER: US 60/232,425

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: CA 2,335,109

PRIOR FILING DATE: 2001-02-23

NUMBER OF SEQ ID NOS: 34

SOPTWARE: PATENTARE: Artificial Sequence

SEQ ID NO 12

LENGTH: 30

TYPE: PAT

ORGANISM: Artificial Sequence

PERIURE:
NAME/KEY: DOMAIN

LOCATION: (15)..(17)

LOCATION: (15)..(17)

COTHER INFORMATION: G's) may be used in variable numbers, such as 2, 3

OTHER INFORMATION: Synthesised in Laboratory:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cashman, Johanne
APPLICANT: Clark-Lewis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILS REFERENCE: SMARO12
FILS REFERENCE: SMARO12
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CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 30
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                                                                                                                                                                                                                                  US-10-086-177A-12
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                                                                                                                                           Sequence 12, Application US/10086177A Publication No. US20030148940A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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FEATURE:
FEA
                                                                              APPLICANT: Tudan,
APPLICANT: Merzov
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APPLICANT: Merzou
APPLICANT: Arab,
                                 APPLICANT:
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TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                           Merzouk, Ahmed
Saxena, Geeta
Eaves, Connie J.
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Eaves, Connie J.
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   Cashman, Johanne
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                                                                                                                  Christopher R.
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Pred. No. 4.8e-1
; Mismatches
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Pred. No. 4.8e-16;
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LENGTH: 30
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Best Local
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                              Query Match
   Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Saxena, Geeta
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100.0%;
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; FEATURE:
; OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) -
; OTHER INFORMATION: 3-SDF-1 (55-67) amide
US-10-086-177A-14
                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-09-39
PRIOR PILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
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CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR TILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2000-02-23
                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 14 LENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/10086177A Publication No. US20030148940A1
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TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
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100.0%; 5
ative 0;
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Pred. No. 4.8e-16;
Mismatches 0;
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Score 169; DB 14; Pred. No. 4.8e-16;

Length 30;

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US-09-835-107-15
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CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 31
                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/09835107
Patent No. US20020165123A1
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Best Local (
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APPLICANT:
APPLICANT:
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  CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
                                                                                                                                                                                                       APPLICANT: Tudan, Christopher R.
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
                                                                               APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
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TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
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                                                                           FILE REFERENCE: SMAR012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (16)..(19)
OTHER INFORMATION: G'spacer monomers (such as the illustrated glycine OTHER INFORMATION: G'spacer monomers (such as the illustrated glycine OTHER INFORMATION: G'spacer monomers (such as the illustrated glycine OTHER INFORMATION: Or 4 glycines.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
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NAME/KEY: DOMAIN
LOCATION: (16)..
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ORGANISM: Artificial Sequence
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Saves, Connie J.
---hman, Johanne
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                                                                                                                                          Cashman, Jo
Clark-Lewis
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Eaves, Connie J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.8%; Score 158.5; DB 9;
larity 96.8%; Pred. No. 1.4e-14;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 2001-02-23
PRIOR FILING DATE: 3001-02-23
NUMBER OF SEQ ID NOS: 34
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Matches 30; Conserv
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APPLICANT:
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PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
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ORGANISM: Artificial Sequence FRATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(18)
COTHER INFORMATION: Grs) may be used in variable numbers, such as 2, 3
OTHER INFORMATION: or 4 glycines.
NAME/KEY: DOMAIN
LOCATION: (24)..(28)
TICOCATION: (24)..(28)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a lactam formation procedure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: SMAR012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 31
TYPE: PRT
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OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017
                                                                                                                                                                                                                                                                            TYPE: PRT
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LOCATION: (31)
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Baves, Connie J.
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Arab, Lakhdar
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Pred. No. 1.4e-14;
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; OTHER INFORMATION:
US-09-835-107-20
                                                                                            US-09-835-107-22
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                                                                                                                RESULT 9
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Best Local S
Matches 30
                                 Sequence 22, Application US/09835107
Patent No. US20020165123A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOPTWARE: PATENTIN Ver. 2.0
SEQ ID NO 21
LENGTH: 31
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APPLICANT: Merzou
APPLICANT: Arab,
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CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
APPLICANT: Tudan, Christopi
APPLICANT: Merzouk, Ahmed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
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LOCATION: (20)..(24)
LOCATION: (20)..(24)
OTHER INFORMATION: Cyclized, for example glutamate (E) and lysine (K)
OTHER INFORMATION: residues may be joined by side chain cyclization
OTHER INFORMATION: using a lactam formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: DOMAIN
LOCATION: (15)..(18)
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated glycine
OTHER INFORMATION: G's) may be used in variable numbers, such as 2,
OTHER INFORMATION: or 4 glycines.
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es 30; Conserv
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Eaves, Connie J.
Tanhman, Johanne
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                 Christopher R
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SDF-1(1-14)-(G)4-SDF(55-67)-E24/K28-cyclic acid
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Pred. No. 1.4e-14;
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Pred. No. 1.4e-14;
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CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
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LENGTH: 31
TYPE: PRT
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CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Application US/09835107
Patent No. US20020165123A1
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Best Local Similarity 96.8%;
                                                                                                                                                                                          APPLICANT: Eaves, Connie J.
APPLICANT: Cashman, Johanne
APPLICANT: Clark-Levis
APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT
FILE REFERENCE: SMARO12
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tudan, Christopher
APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
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LOCATION: (24)..(28)

LOCATION: (24)..(28)

OTHER INFORMATION: Cyclized, for example (E) and lysine (K) residues

OTHER INFORMATION: may be joined by side chain cyclization using a

OTHER INFORMATION: lactem formation procedure.

OTHER INFORMATION: Synthesised in Laboratory:

OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-E24/K28-cyclic

OTHER INFORMATION: amide: or CTCE0022
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TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
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LOCATION: (15)..(18)

OTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: or 4 glycines.
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Eaves, Connie J.
Cashman, Johanne
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Eaves, Connie J.
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Pred. No. 1.4
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PatentIn Ver. 2.0

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APPLICANT: Salari, Hassan
APPLICANT: Salari, Hassan
FILE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAROL2
CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 31
TYPE: PRT
ORGANISM: Artificial Sequence
PRATURE:
PR
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Best Local Similarity
Matches 30; Conserv
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SOFTWARE: PatentIn Ver. 1
SEQ ID NO 23
LENGTH: 31
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APPLICANT: Merzouk, Ahmed
APPLICANT: Arab, Lakhdar
APPLICANT: Saxena, Geeta
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NAME/KEY: DOMAIN

LOCATION: (15)..(18)

COTHER INFORMATION: spacer monomers (such as the illustrated glycine OTHER INFORMATION: G's) may be used in variable numbers, such as 2, OTHER INFORMATION: or 4 glycines.

NAME/KEY: DISULFID LOCATION: (9)..(11)

COTHER INFORMATION: cystein residues may for example be involved in OTHER INFORMATION: bridge formation
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LOCATION: (15)..(18)
COTHER INFORMATION: g's) may be used in variable numbers, such as 2,
OTHER INFORMATION: or 4 glycines.
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LOCATION: (20)..(24)
OTHER INFORMATION: C
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6, Application US/09835107
US20020165123A1
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Arab, Lakhdar
Saxena, Geeta
Baves, Connie J.
Cashman, Johanne
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larity 96.8%;
Conservative
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SDF-1(1-14)-(G)4-SDF-1(55-67)-K20/E24-cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 158.5; DB 9;
Pred. No. 1.4e-14;
D; Mismatches 0;
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RESULT 13 US-10-086-177A-13

Sequence 13, Application US/10086177A Publication No. US20030148940A1 GENERAL INFORMATION:

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                                                                                                                                     US-09-835-107-27
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                                                                                 Query Match
Best Local (
                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                              LOCATION: (9)..(11)
OTHER INFORMATION: Cysteine residues may for example be invloved in OTHER INFORMATION: bridge formation.
OTHER INFORMATION: Synthesised in Laboratory:
OTHER INFORMATION: SDF-1(1-14)-(G)4-SDF-1(55-67)-C9/C11-cyclic amide NAME/KEY: MOD RES
LOCATION: (31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn
EQ ID NO 27
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/835,107
CURRENT FILING DATE: 2001-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
FILE REFERENCE: SMAR012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Tudan,
APPLICANT: Merzou
APPLICANT: Arab,
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: DOWAIN
LOCATION: (15)..(18)
OTHER INFORMATION: spacer monomers (such as the illustrated OTHER INFORMATION: G's) may be used in variable numbers, suc OTHER INFORMATION: or 4 glycines.
                                                                                                                                                   OTHER INFORMATION: AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 30; Conserv
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                                                                30;
                              1 KPVSLSYRCPCRFF-GGGLKWIQEYLEKALN 30
                                                                                 Similarity
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Eaves, Connie J.
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320020165123A1
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                                                                Conservative
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                                                                                 93.8%;
                                                                0; Mismatches
                                                                                 Score 158.5; DB 9
Pred. No. 1.4e-14;
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Pred. No. 1.4e-14;
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PPLICANT: Tudan, Christopher R.

Saxena, Geeta Eaves, Connie J.

Clark-Lewis, Ian

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FILE REFERENCE: SMAR-012CIP
CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/835,107
PRIOR FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/232,425
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR APPLICATION NUMBER: CA 2,335,109
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                                                                                               PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PASTSEQ for Windows
SEQ ID NO 15
LENGTH: 31
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Best Local
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TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 31
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PRIOR FILING DATE: 2001-04-12
PRIOR PELLING DATE: 2001-04-12
PRIOR PELLING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR PILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR PELLING DATE: 2000-04-12
PRIOR PELLING DATE: 2000-04-12
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CURRENT FILING DATE: 2002-02-26
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TITLE OF INVENTION: CXCR Agonist Treatment of Hematopoietic
TITLE OF INVENTION: Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                             FEATURE:
                                               ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthesized in Laboratory: SDF-1 (1-14) -
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Local Similarity 96.8%;
as 30; Conservative
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Eaves, Connie J.
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Clark-Lewis, Ian
                                                                                                                                                         for Windows Version 4.0
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Pred. No. 1.4e-14;
0; Mismatches 0;
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Search completed: January Job time: 97.8689 secs

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2005, 16:04:59

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                                                                                                                                    ; TYPE: PRT; ORGANISM: Artificial Sequence; PEATURE: TIPORMATION: Synthesized in Laboratory: SDF-1; OTHER INFORMATION: 4-SDF-1 (55-67) - E24/K28-Cyclic US-10-086-177A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-086-177A-20
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                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/086,177A
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: 09/335,107
PRIOR FILING DATE: 2001-04-12
PRIOR PELING DATE: 2001-04-12
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: CA 2,305,036
PRIOR APPLICATION NUMBER: CA 2,335,109
PRIOR FILING DATE: 2001-02-23
                                                                 Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                           SEQ ID NO 20
LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/100 Publication No. US20030148940A1
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Salari, Hassan
TITLE OF INVENTION: CXCR Agonist Treatment
TITLE OF INVENTION: Cells
FILE REFERENCE: SMAR-012CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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KPVSLSYRCPCRFFGGGGLKWIQEYLEKALN
                   KPVSLSYRCPCRFF-GGGLKWIQEYLEKALN 30
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Eaves, Connie J.
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                                                                    Conservative
                                                                                 93.8%;
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Pred. No. 1.4e
0; Mismatches
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                                                                                 Score 158.5; DB 14; Pred. No. 1.4e-14;
                                                                    0; Mismatches
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	GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - pr	OM protein - protein search, using sw model
Run on:	January 4, 2005, 15:43:59; Search time 12.2951 Seconds (without alignments) 234.769 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-086-177A-12 169 1 KPVSLSYRCPCRFFGGGLKWIQEYLEKAIN 30
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	283416 segs, 96216763 residues
Total number of	Total number of hits satisfying chosen parameters: 283416
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	PIR 79:* 1: pir1:* 2: pir2:* 3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ហ	4	ω	2	_	Result No.	
47	47	47.5	47.5	48	48	48.5	48.5	49	49	49	49	49.5	49.5	49.5	49.5	49.5	49.5	50.5	52	54.5	54.5	56.5	S	59.5	ന	118.5	118.5	118.5	Score	
27.8		28.1	8	8	28.4	28.7	28.7	9	9	29.0	9	9	9	29.3	9	29.3	9	29.9		۲.	32.2	·	ū	35.2	70.1	70.1	70.1	70.1	Query Match	
390	311	378	212	340	312	1429	685	577	439	347	340	1147	588	557	556	469	189	3433	974	1400	233	1081	1088	1084	93	93	89	89	Length	
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873635	H71252	T11713	S73466	T23492	T23493	S06434	T10800	I50731	E72298	I51546	I51547	T42627	S34786	A25493	A53376	C83345	D69389	GNWVKV	T10797	T22644	T35594	T52028	H84604	T08583	181182	G01540	A53497	I53416	ID	
kinas		probable alpha-1,2			cal prot	homeotic protein l	cellulose synthase	Ig heavy chain - n	hypothetical prote	probable RNA-bindi	probable RNA-bindi	ADP-ribosylation f	catechol oxidase (tryptophan 2-monoo	tryptophan 2-monoo	probable class III	DNA-directed RNA p	genome polyprotein	cellulose synthase		hypothetical prote		probable cellulose	cellulose synthase	cytokine - mouse	cytokine SDF-1-bet	pre-B-cell growth-	leukin-8 ho	Description	

ALIGNMENTS

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C;Species: Mus sp. (mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: IS3416
R;Jiang, W.; Zhou, P.; Kahn, S.M.; Tomita, N.; Johnson, M.D.; Weinstein, I.B.
Exp. Cell Res. 215, 284-293, 1994
A;Title: Molecular cloning of TPAR1, a gene whose expression is repressed by the tumor A;Reference number: IS3416; MUID:95073497; PMID:7982471
A;Accession: IS3416
A;Cross-references: UNIPROT:P40224; GB:D21072; NID:g413905; PIDN:BAA04648.1; PID:g46845 R;Tashiro, K.; Tada, H.; Heilker, R.; Shirozu, M.; Nakano, T.; Honjo, T. Science 261, 600-603, 1936 Science 261, 600-603, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Nagasawa, T.; Kikutani, H.; Kishimoto, T.
Proc. Natl. Acad. Sci. U.S.A. 91, 2305-2309, 1994
A;Title: Molecular cloning and structure of a pre-B-cell growth-stimulating factor.
A;Reference number: A53497; MUID:94181581; PMID:8134392
A;Accession: A53497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pre-B-cell growth-stimulating factor precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004 C;Accession: A53497; 159582
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C;Superfamily: beta-thromboglobulin
                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-89 <NAG>
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A;Molecule type: mRNA
A;Residues: 1-89 <RES>
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Best Local Similarity 40.3%;
Matches 27; Conservative
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Pred. No. 3.5
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3.5e-09;
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A;Gene: :
C;Superf:
C;Keyword
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submitted to the EMBL Data Library,
".pafarence number: G07697
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                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-93 < RES>
                                                                                                                                                         A;Title: Signal sequence trap: a cloning strategy for secreted proteins and A;Reference number: I59582; MUID:93342488; PMID:8342023 A;Accession: I81182
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C;Species:
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A; Residues: 1-93 < SPO>
A; Cross-references: UNIPROT: P48061; EMBL: U16752; NID: g1272194; PID: g571508
C; Superfamily: beta-thromboglobulin
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C;Accession: G01540
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Matches 27
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;Accession: I81182
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Superfamily: beta-thromboglobulin
                                                       Superfamily: beta-thromboglobulin
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Best Local
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                                                                                               UNIPROT: P40224; GB:L12030; NID: g393181; PIDN: AAA40101.1; PID: g393182
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Pred. No. 3.5e
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Score 118.5; DB 2;
Pred. No. 3.6e-09;
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A; Gene
A; Map
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Introns: 27/3;
C; Keywords: 27/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellulose synthase (BC 2.4.1.-) catalytic chain - A NyAlternate names: protein T22F.250 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 C;Accession: T08583; T09014
                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1088 <STO>
                                                                                                                                                                                                                                                                                                                                                          probable cellulose synthase catalytic subunit [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:048947; EMBL:AL050351; GSPDB:GN00062; ATSP:T2278.250
A;Experimental source: cultivar Columbia; BAC clone T2278
R;Arioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wittke, W.; Herth, W.; Camiller Science 279, 717-720, 1998
A;Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A;Reference number: Z13745; MUID:98111412; PMID:9445479
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A;Residues: 1-1084 <ARI>
A;Cross-references: EMBL.AF027173; NID:g2827140; PIDN:AAC39335.1; PID:g2827141
A:Rxnerimental source: cultivar Columbia
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                                                            Gene: At2g21770;
Map position: 2
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                                                                                                                      Cross-references:
                                                                                                                                                                                                    Accession: H84604
                                                                                                                                                                                                                                                                                                                                           Accession: H84604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene: ATSP:T22F8.250; Ath-A
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Query Match
Best Local Similarity
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Similarity 43.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                      UNIPROT: Q9SJ22;
  35.2%;
43.5%;
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  Score
Pred.
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Pred. No. 4.1;
                                                                                                                      GB:AE002093; NID:g4417271;
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  159.5; DB
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May 1999
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                    Length 1088;
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hypothetical protein F54D1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22644
R;Lennard, N.
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T52028
                                                                       submitted to the EMBL Data Library, July 1996 A; Reference number: Z19592 A; Accession: T22644
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T35594
R;Saunders, D.; Harris, D.; Parkhill, J.; Barrell, B.G.; submitted to the EMBL Data Library, August 1998
A;Reference number: Z21583
A;Accession: T35594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SC6G4.43c SC6G4.43c - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
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A;Residues: 1-1081 <JOS>
A;Cross-references: UNIPROT:O65338; EMBL:AF062485; PIDN:AAC29067.1
                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1400 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, May 1998
A;Reference number: Z25890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulose synthase [imported] - Arabidopsis thaliana (fragment)
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;Cross-references: UNIPROT:O86804;
;Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: Arabidopsis thaliana (mouse-ear cress);Date: 20-Oct-2000 #sequence_revision 20-Oct-2000;Accession: T52028
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: hypothetical protein HI0278;
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 32.2%;
Best Local Similarity 40.0%;
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Best Local
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 Cross-references: UNIPROT:Q20766;
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IFLSRHCPIWYGYGGGLKWLERF 859
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                                                                                                                                                                                                                                                                                                                                    SYRCPCRFFGGGL---KWIQEYLEK 27
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Pred. No. 11
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EMBL: Z77132; PIDN: CAB00861.1; GSPDB: GN00022; CESP: F5
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 233;
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A;Gene: CESP:F54D1.5
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Best Local
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A; Cross-references: UNIPROT: P14335; GB: D00246; NID: g221966; PIDN: BAA00176.1; PID: g2
C; Superfamily: yellow fever virus genome polyprotein
C; Keywords: ATP; capsid protein; envelope protein; membrane protein; nonstructural
F;2-123) Product: capsid protein C #status predicted <CPC>
F;124-290/Product: membrane protein M precursor #status predicted <MPP>
F;124-290/Product: membrane protein M sequence #status predicted <SIG>
F;216-290/Product: membrane protein M #status predicted <NEM>
F;216-290/Product: membrane protein B #status predicted <NEM>
F;291-791/Product: nonstructural protein NS1 #status predicted <NS1>
F;1144-1374/Product: nonstructural protein NS2 #status predicted <N2A>
F;1375-1505/Product: nonstructural protein NS2 #status predicted <N2B>
F;1506-2124/Product: nonstructural protein NS3 #status predicted <N2B>
F;1506-2124/Product: nonstructural protein NS3 #status predicted <N2B>
                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Coia, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.
J. Gen. Virol. 69, 1-21, 1988
A;Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene A;Reference number: A28697; MUID:88089524; PMID:2826659
A;Accession: A28697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Kunjin virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genome polyprotein - Kunjin virus (strain MRM61C)
N;Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural
in NS4a; nonstructural protein NS4b; nonstructural protein NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Pear, J.R.; Kawagoe, Y.; Schreckengost, W.E.; Delmer, D.P.; Stalker, D.M. Proc. Natl. Acad. Sci. U.S.A. 93, 12637-12642, 1996
A;Title: Higher plants contain homologs of the bacterial celA genes encoding A;Reference number: Z17152; MUID:97057296; PMID:8901635
A;Accession: T10797
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                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: genomic RNA
A; Residues: 1-3433 <COI>
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A;Experimental source: strain Acala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
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RESULT 13
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A;Residues: 1-469 <STO>
A;Cross-references: UNIPROT:Q91168;
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A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: D69389
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F;1786-1791/Region: nucleotide-binding moti
F;1790-1793/Region: DEAH motif
F;2125-2271/Product: nonstructural protein
F;2274-2528/Product: nonstructural protein
F;2529-3433/Product: nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary A; Molecule type: DNA
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Nature 390, 364-370, 1997
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C; Accession:
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C;Species: Archaeoglobus fulgidus
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;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                  Query Match
Best Local
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Accession: D69389
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Pred. No. 46
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Pred. No. 2e+02;
5; Mismatches 12;
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irkness, E.F.
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Search completed: January Job time: 13.2951 secs

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RESULT 15
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C;Species: Pseudomonas syringae pv. savastanoi
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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A;Residues: 1-557 <YAM>
A;Cross-references: UNIPROT:P06617
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Proc. Natl. Acad. Sci. U.S.A. 82, 6522-6526, 1985
A;Title: Nucleotide sequences of the Pseudomonas savastanoi indoleacetic acid genes show
A;Reference number: A94062
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A; Residues: 1-556 < MAZ>
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J. Bacteriol. 176, 1374-1382, 1994
A;Title: A mutation in the indole-3-acetic
A;Reference number: A53376; MUID:94156842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A53376
                                                                                                                                                                                                                                                                              A; Accession: A25493
                                                                                                                                              ;Superfamily: Pseudomonas tryptophan 2-monooxygenase;Keywords: monooxygenase; oxidoreductase
                                                                                                                                                                                   Gene: iaaM
                                                                       Query Match
Best Local Similarity
Matches 10; Conservat
                                                                                                                                                                                                     Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Date: 10-Sep-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           iaaM
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511 CSCSFAGG---WIEGAVQTALN
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                                   CPCRFFGGGLKWIQEYLEKALN 30
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3; Mismatches
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PMID:8113177
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1: uniprot_sprot:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Bac35845 mus muscu
Cag29279 homo sapien
09h554 homo sapien
062657 felis silve
P48061 homo sapien
06cekw4 sus scrofa
080zw4 mus musculu
06t7c0 gallus gall
Aar88102 gallus gall
Aar91695 gallus gall
Aar91695 gallus gal
09czd1 rattus norv
08uuj9 xenopus la
09gzd1 rattus norv
08uuj9 xenopus la
09gzd7 rattus norv
08uuj9 xenopus la
09gy78 ratiospis
049377 arabidopsis
049378 arabidopsis
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049378 arabidopsis
050955 brachydanio
04070701 escherichia
Cae85184 escherichia
07c09 shigella fl
083jq0 shigella fl
083jq0 shigella fl
086fkt6 escherichia
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Q8hyp0 macaca mula
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RC STRAIN-C57BL/6J; TISSUE-Mammary gland;
RC STRAIN-C57BL/6J; TISSUE-Mammary gland;
RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Willahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Rillaion D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA William M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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A Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

A Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

A Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.S., Ringwald M.,

Ra Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.S., Ringwald M.,

Ra Sandelin A., Schneider C., Semple C.A., Serou M., Shimada K.,

Ra Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,

Ra Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

Ra Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Ra Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Ra Ahiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,

Ra Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

Para Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Para Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Analysis of the mouse transcriptome based 60,70 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          not neutrophile.

FUNCTION: Stimulates the proliferation of bone marrow-derived progenitor cells in the presence of IL-7 as well as growth of stromal cell-dependent B-cell clone DW34 cells.

SUBCELULIAR LOCATION: Secreted.

ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;
L11072; BAAA04648.1; --
L12029; AAA40100.1; --
L12030; AAA40101.1; --
L5; S74318; AAB32650.1; --
L5; D43804; BAA07862.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P40224-2; Sequence=VSP_001057; SIMILARITY: Belongs to the intercrine alpha (chemokine CxC)
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FUNCTION: Chemoattractant active on T-lymphocytes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name-Beta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family.
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                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.
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Best Local S
Matches 27
Query Match
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MGD; MGI:103556; CXcl12.

GO; GO:0008009; F:chemokine activity; IDA.

GO; GO:0007420; P:brain development; IDA.

GO; GO:0007420; P:regulation of cell migration; IDA

GO; GO:0042098; P:T-cell proliferation; IMP.

InterPro; IPR002473; C-X-C/Interlkn_8.

InterPro; IPR001811; Chemokine_IBB.

InterPro; IPR001811; Chemokine_IBB.

InterPro; IPR001811; Chemokine_smll.

Pfam; PF00048; ILB; 1.
                                                                                                                                                                                                                                                                                                                                                                                         Q8HYP0
Q8HYP0;
01-MAR-2003
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                                                                                                                                                                     MEDIINE=22123042; PubMed=12126650;
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Molecular cloning and sequencing of 25 different rhesus macaque
chemokine cDNAs reveals evolutionary conservation among C, CC, CX
AND CX3C families of chemokines.";
Cytokine 18.140-148(2002).
                                                                                                                                                                                                                                                                              Cercopithecinae, Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00471; SMALL CYTOKINES CXC; FALSE NEG.
Alternative splicing; Chemotaxis; Tytokine; Growth factor; Signal.
SIGNAL
1 21 Potential
CHAIN
22 89 Stromal cell-derived factor 1.
DISULFID 30 55 By similarity.
DISULFID 32 71 By similarity.
VARSPLIC 89 89 K.-> KRLKM (in 1soform Beta).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                    Chemokine CXCL12/SDF-1ALPHA.
                                                                 Pfam;
                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR002473; C-X-C/Interlkn.8.
InterPro; IPR001811; Chemokine_ILB.
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BC006640; AAH06640.1;
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                                PR00436; INIL.
                                        SM00199;
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40.3%;
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By similarity.
K -> KRLKM (in iso:
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Pred. No. 1.3e-09;
0; Mismatches 3
Score 118.5; DB 2; Length 89;
                          AD531633C6DC2B07 CRC64;
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                                                                                                                                                                                                                           CAC10203;
02-MAR-2004
02-MAR-2004
02-MAR-2004
BA20J15.1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE TISSUE=thymus;
Nishimura Y., Miyazawa T., Ikeua .
Nishimura Y., Miyazawa .
Ni
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                                                                     Bird
                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Carnivora;
   SEQUENCE
                                                     Submitted (SEP-2000)
                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                   CAC10203
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                                    EMBL; AL137026;
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                                                                                         FROM N.A.
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(TrEMBLrel. 27, Last s
(Stromal cell-derived
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                                  CAC10203.1;
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                                                                                                                                       Chordata;
Primates;
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Pred. No. 1.3e-09;
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STROMAL CELL-DERIVED FACTOR-1A.
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; Fissipedia;
                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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 62B44E8D209C3A14 CRC64
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                  Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN=C57BL/GJ; TISSUE=Parthenogenote;

MEDLINE=20499374; PubMed=11042159;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibat Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

"Normalization and subtraction of cap-trapper-selected prepare full-length cDNA libraries for rapid discovery genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-C57BL/60; TISSUE-Parthenogenote;
MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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BAC32216;
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STRAIN=C57BL/6J; TISSUE=Parthenogenote;
MEDLINE=21085660; PubMed=11217851;
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STRAIN=C57BL/6J; TISSUE=Parthenogenote,
MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Parthenogenote; MEDLINE=20530913; PubMed=11.076861; Ctille:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Analysis of the mouse transcriptome based 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation
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Mammalia; Eutheria;
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APR-2004 (TrEMBIrel. 27, Last sequence update)
APR-2004 (TrEMBIrel. 27, Last annotation update)
APR-2004 (TrEMBIrel. 27, Last annotation update)
days embryo parthenogenote CDNA, RIKEN full-length
rary, clone:B13003ZA21 product:stromal cell derived
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Pred. No. 1.3e-09;
0; Mismatches 3;
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Sciurognathi; Muridae;
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Matches 27
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A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Kurihara C., Matsuyama T., Miyazaki A., Murate M., Nakamura M.,
A Kurihara C., Matsuyama T., Miyazaki A., Murate M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
L Submitted (UJU-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL, AK045092; BAC32216.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based o 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                  SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Kidney;
MEDLINE-99279253; PubMed-10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA,
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
Eukaryota, Metazoa;
Mammalia; Eutheria;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last samotation update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
Adult male kidney cDNA, RIKEN full-length enriched library,
clone:0610039H13 product:stromal cell derived factor 1, full insert
                                                                                                                                                                                                                                                                                     Nature
[3]
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217851;
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Parthenogenote;
Akimura T., Araka
                                                                                                                                                                                                                                                                                                              RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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27, Conserv
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Pred. No. 1.
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Sciurognathi; Muridae;
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  Shibata K.,
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RESULT 7
CAG29279
ID CAG2
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A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Shinagawa A., Shiraki T.,

A Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai K.,

A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Sogabe Y., Toya T., Yamamura T., Yamanaka I., Yasunishi A.,

Yoshida K., Yoshino M., Miramateu M., Hayashizaki Y.,

Submitted (Apr-2002) to the EMBL/GenBank/DDBJ databases.
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                   EMBL;
                                                                                                                                                                                                                                          CAG29279;
20-MAY-2004
20-MAY-2004
20-MAY-2004
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Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara S., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                     vector (pr
Submitted
                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                            SEQUENCE
                                                                                                                                                                                                                                                                                                     CAG29279
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                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                   Homo sapiens
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                                                                                                "Cloning
                                                                  L., Schick M., Neubert ing of human full open r (pDONR201)."; to the E
                                                      CR450283; CAG29279.1;
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//6J; TISSUE=Kidney;

Akahira S.
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Primates;
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 70.1%;
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Pred. No. 1.3e
0; Mismatches
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Last annotation update)
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 Score 118.5;
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                            62B44E8D209C3A14
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Gateway (TM)
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Hori F.,
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RESULT 9
SDF1_FELCA
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01-JUN-2003
BA20J15.1.2
                                                                                                                                                                              Capfi FELCA STANDARD, PRT; 93 AA. 062657;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Stromal cell-derived factor 1 precursor (SDF-1)
Name=CXCL12; Synonyms=SDF1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; II
GO; GO:0006955; F:immune response; IEA.
InterPro; IPR002473; C-X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
PRINTS; PR00436; INTERLEUKIN8.
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SEQUENCE FROM N.A. (ISOFORMS ALPH
TISSUE=Thymus;
MEDLINE=98450506; PubMed=9777331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                              Name=CXCL12; Synonyms=SDF1;
Felis silvestris catus (Cat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0436; INTERLE SMART; SM00199; SCY; 1.
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(TrEMBLrel. 24, Last annotation update)
(Stromal cell-derived factor 1, isoform beta)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                 (ISOFORMS ALPHA
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0; Mismatches 3;
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Pred. No. 1.4e-09;
0; Mismatches 3;
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                                                                                                                   Euteleostomi; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GLKWIQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GLKWIQE
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RESULT 10
SDF1_HUMAN
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                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                               SDF1_HUMAN
P48061;
01-FEB-1996
                                                                                01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Stromal cell-derived factor 1 precursor (SDF-1) (CXCL12) (Pre-B cell growth stimulating factor) (PBSF) (hIRH) [Contains: SDF-1-beta(3-72);
SDF-1-slpha(3-67)].
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura Cai J.S., Sato B., Kohmoto M., Mikami T.; "Mòlečulaf cloning and sequencing of feline stromal cell-d factor-1 alpha and beta.";
                                  Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB011966;
HSSP; P48061; 19
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                       Name=CXCL12; Synonyms=SDF1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002473; C-X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_IL8.
InterPro; IPR001089; CCC_chmkine_smll.
Pfam; PF00048; IL8; 1.
SEQUENCE FROM N.A
                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION:
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . J. Immunogenet. 25:303-305(1998). FUNCTION: Chemoattractant active on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family.
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                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM00199; SCY;
                                                                                                                                                                                                                                                                                                                                                                                                      ive splicing; Chemotaxis; Cytokine; Growth factor; Signal.

1 21 Potential.
22 93 Stromal cell-derived factor;
30 55 By similarity.
31 71 By simil
                                                                                                                                                                                                                                                       YLEKALN
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR00436;
                                                                                                                                                                                                                                                                                         KPVSLSYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQE
                                                                                                                                                                                                                                                                                                           KPVSLSYRCPCRFFGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00471;
                                                                                                                                                                                                                                        YLEKALN
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAA28602.1;
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                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                     70.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence=VSP_001055;
ys to the intercrine alpha (chemokine CxC)
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Me:
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                                                                                                                                                                                                                                                                                                                                                                                         Stromal cell-derived factor 1
By similarity.
By similarity.
Missing (in isoform Alpha).
/FTId=VSP 001055.
/#4FC7637IIE9BE37 CRC64;
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                                                                                                                                                                                                                                                                                                                                                     Score 118.5;
Pred. No. 1.4
                                   Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                          93
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                                      Hominidae;
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RA Deloukas P., Earthrowl M.E., Grafham D.V., Rubenfield M., French L.,
RA Steward C.A., Sims S.K., Jones M.C., Searle S., Scott C., Howe K.,
RA Hunt S.E., Andrew T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA Hunt S.E., Andrew T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA Hunt S.E., Andrew T.D., Gilbert J.G.R., Swarbreck D., Ashurst J.L.,
RA Hunt S.E., Ambrose K.D., Babbage A.K., Bagguley C.L., Bailey J.,
RA Ashwell R.I.S., Ambrose K.D., Babbage A.K., Bagguley C.L., Bailey J.,
RA Banerjee R., Bates K., Beasley H., Bray-Allen S., Brown A.J.,
RA Banerjee R., Bufford D.C., Burrill W., Burton J., Cahill P., Camire D.,
RA Carter N.P., Chapman J.C., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
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RA Carter N.P., Chapman J.C., Johnson E., Hammond S., Harley J.L.,
RA Frankish A., Frankishd J.A., Garner P., Garnett J., Gribble S.,
RA Griffiths C., Grocock R., Gustafson E., Hammond S., Harley J.L.,
RA Hurk E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
RA Hurk E., Hynds C., Johnson C., Johnson D., Kana A., Kay M.,
RA Kimberley A.M., Kershaw J.K., Kokkinaki M., Laird G.K., Lawlor S.,
RA Loveland J., Lovell J., McLaren S., McLay K.E., McMurray A.,
RA Mashreghi-Mohammadi M., Matthews L., Milne S., Nickerson T.,
RA McLarter M., Chern H.K., Shownkeen R., Skuce C.M., Rogosin A., Ross M.T.,
RA Pelan S., Phillimore B., Porter K., Rice C.M., Rogosin A., Ross M.T.,
RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilning L.,
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RA Weinstock K., West A.P., Willey D.L., Whitehead S.L., Wilning L.,
RA Waray P.W., Young L., Chen Y., Lovering R.C., Moschonas N.K.,
RA Moschonas M.K., Senthe D.R., Rogers J.,
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                                                                                              REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altechnil S.F. Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechnil S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (2)
SEQUENCE FROM N.A.
MEDLINE-96039262; PubMed=7490086;
                                               and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM ALPHA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1994) to
  IDENTIFICATION
  ဝှု
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOI=10.1038/nature02462; throwl M.E., Grafham D.V.,
SDF-1ALPHA (3-67)
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AND
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SDF-1BETA (3-72)
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BY MASS
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SPECTROMETRY, AND N-TERMINAL AND C-TERMINAL PROCESSING.
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"Differential processing of stromal-derived factor-lalpha and beta
explains functional diversity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98046030; PubMed=9384579;
Crump M.P., Gong J.H., Loetscher P., Ra;
Arenzana-Seisdedos F., Virelizier J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MEDLINE=98284037; PubMed=9618518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Solution structure and basis for derived factor-1; dissociation of inhibition of HIV-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          derived factor lalpha,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRUCTURE BY NMR OF 22-88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of chemically synthesized [N33A] stromal derived factor lalpha, a potent ligand for the HIV-1 'fusin'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 16:6996-7007(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reduced chemotactic activity. Binding to cell surface proteoglycans seems to inhibit formation of SDF-1-alpha(3-67) at thus to preserve activity on local sites.

SUBCELLULAR LOCATION: Secreted.

ALTERNATIVE PRODUCTS:
Event-Alternation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isofor Name=Beta; Synonyms=SDF-1-beta(1-72); IsoId=P48061-1; Sequence=Displayed; Name=Alpha; Synonyms=SDF-1-alpha(1-68); IsoId=P48061-2; Sequence=VSP 001056; PTM: Processed forms SDF-1beta(3-72) and
                                                                                                                                                                                                                                                                                                                                                                 proteoglycans SIMILARITY: Be
                                                                                                                                                                                                                                                                                                                                                                                                      PTM: Processed forms SDF-1beta(3-72) and SDF-1alpha(3-67) are produced after secretion by proteolytic cleavage of isoforms Beta and Alpha, respectively. The N-terminus processing is probably achieved by DPP4. Isoform Alpha is first cleaved at the C-terminus to yield a SDF-1-alpha(1-67) intermediate before being processed at the N-terminus. The C-terminal processing of isoform Alpha is
                                                                                                                                                                                                                                                                                                                                                   family.
                                                                                                                                                                                                                                                                                                                                                                                          reduced by binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103:2452-2459(2004).
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                                                                                                                                                                                                                                                                                                                                                                                            heparin and,
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L., Baggiolini M.,
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                                                                                                                                                                                                                                                                                                                                                                 (chemokine CxC)
                                                                                                                                                                                                                                                                                                                                                                                            cell surface
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J5; AA.

J37026; CA.

BC039893; AAH3.

A; G01540; G01540.

PDB; 1A15; X-ray; A'

PDB; 1QG7; X-ray'

DR PDB; 1SDF; NMP

DR PDB; 2SDF; NMP

DR Genew; HC'

MIM; 6'

GO; EMBL; U16752; AAA97434.1; -.
EMBL; L36033; AAB39332.1; -.
EMBL; L36034; AAB39333.1; -.
EMBL; U19495; AAB46516.1; -.
EMBL; AL137026; CAC10203.1; -.
EMBL; BC039893; AAH39893.1; -. entities or send a This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and GO: 0008009; GO: 0005102; GO: 0006874; an requires a license agreement (S an email to license@isb-sib.ch). ; X-ray; A/B=22-88. ; X-ray; A/B=22-88. ; NMR; @=22-88. ; NMR; @=22-88. F:chemokine activity; T)
F:receptor binding; TAS
P:calcium ion homeostas: CXCL12. (See http://www.isb-sib.ch/announce/ restrictions and EMBL a collaboration outstation 9

homeostasis;

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ACCOCC OF THE REAL PROPERTY OF
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Q6EKW4
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SEQUENCE
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STRAND
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           Ledger T.N., Pinton P., Bourges D., Roumi P.
"Development of a macroarray to specifically
gene expression in Swine.";
Clin. Diagn. Lab. Immunol. 11:691-698(2004).
EMBL; AY312066; AAQ88094.1;
                                                                                                                                                                                                                                             01-OCT-2004 (TrEMBLrel.
01-OCT-2004 (TrEMBLrel.
01-OCT-2004 (TrEMBLrel.
CXCL12 chemokine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TURN
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                                                                                                   SEQUENCE FROM N.A.
PubMed=15242943;
                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                               Name=CXCL12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00048; IL8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001811; Chemokine_IL8.
InterPro; IPR001089; CXC_chmkine_smll.
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                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                     Q6EXW4;
                                                                                                                                                                                                                                                                                                                                    Q6EKW4
                                                                                                                                                       NCBI_TaxID=9823;
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GO:0006935; P:chemotaxis; TAS.
GO:0006015; P:circulation; TAS.
GO:0007186; P:G-protein coupled receptor protein signalin. .
GO:0007186; P:mmune response; TAS.
GO:0008064; P:regulation of actin polymerization and/or d. .
GO:0009615; P:response to virus; TAS.
GO:0009615; P:signal transduction; TAS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPVSLSYRCPCRFFGG----
116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                  Bourges D., Roumi P., array to specifically
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Last annotation updat
                                                                                                                                                                                                                                                                                                 Created)
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Pred. No. 1.4e
0; Mismatches
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2A1BCE0551C2BEAB CRC64;
                                                                                                                                                                                                                                                                                                                                      116
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1.4e-09;
3;
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analyze
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                                                                                                                                                                                            Euteleostomi;
                                                                                  Ή;
                                                                      immunological
                                                                                    Oswald
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RESULT
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AMEDILINE-2238857; PubMed-12477932;

AS Strausberg R.D., Peingold E.A., Grouse L.H., Derge J.G.,

AR Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

AR Klausner R.D., Collins F.S., Wagner L., Shenfer C.F., Bhat N.K.,

AR Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Blackelin M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Basa S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hullyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Wilting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

RA Moltiguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Matches
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                                                                                        GO; GO:0008009; F:Chemokine activity; IDA.
GO; GO:0007420; P:brain development; IDA.
GO; GO:0007420; P:brain development; IDA.
GO; GO:0008354; P:germ cell development; IDA.
GO; GO:0008354; P:germ cell migration; IDA.
GO; GO:0050930; P:induction of positive chemotaxis; IDA.
GO; GO:0050930; P:positive regulation of cell migration; IDA.
GO; GO:0042098; P:T-cell proliferation; IMP.
InterPro; IPR002473; C-X-C/Interlkm 8.
InterPro; IPR001811; Chemokine_IL8.
                                             PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2003
01-JUN-2003
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Mammalia; Eutheria;
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STRAIN=C57BL/6; TISSUE=Brain;
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                                SEQUENCE
                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                          Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                      "Generation and initial analysis and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                        ones S.J., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
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MGI:103556; Cxcl12.
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                                               PR00436; INT
SM00199; SCY;
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                                AA;
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                                15529 MW;
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24,
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Last sequence update)
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Pred. No. 1.7e-09;
0; Mismatches 3
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                                04B47DAB6904DF77 CRC64;
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Length 137;
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Query Match

70.1%;

Score 118.5;

DB 2;

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RESULT 14
AAR88102
ID AAR88102;
AC AAR88102;
DT 02-MAR-20
DT 02-MAR-20
DT 02-MAR-20
DE Stromal c
GN SpP1.
OS Gallus ga
OC Bukaryota
OC Archosaur
OC Gallus.
OX NCBI TaxI
RN [1]
RP SEQUENCE
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Matches 2
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TISSUB-Spleen;
Read L.R., Cumberbatch J., Sharif S.;
Read L.R., Cumberbatch J., Sharif S.;
Submitted (CCT-2003) to the EMBL/GenBank,
EMBL; AY429472; AAR91695.1; -.
EMBL; AY451855; AAR91695.1; -.
EMBL; AY451855; AAR91695.1; -.
InterPro; IPR002473; C.X-C/Interlkn_8.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
PRINTS; PR00436; INTERLEUKIN8.
SMART; SM00199; SCY; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 89 AA; 10104 MW; 21E53D121A
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02-MAR-2004 (TrEMBLrel. 27,
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02-MAR-2004 (TrEMBLrel. 27,
Stromal cell derived factor
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
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05-JUL-2004 (TrEMBLrel. 27, Last sequence up
05-JUL-2004 (TrEMBLrel. 27, Last annotation
Stromal_cell-derived factor-1 alpha.
                   Gallus.
NCBI_TaxID=9031;
                                             Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; (
Archosauria, Aves; Neognathae;
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Raz E., Stebler J.;
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Neognathae; Galliformes; Phasianidae; Phasiani
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RAZ E., Stebler J.;

"Chicken SDF-1alpha.";

"Chicken SDF-2003) to the EM
Submitted (OCT-2003) to the EM
EMBL; AY429472; AAR91695.1; -.

SEQUENCE 89 AA; 10104 MW;
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AAR91695;
14-APR-2004
14-APR-2004
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14-APR-2004 (TrEMBLrel. 27, Last annotation
Stromal cell-derived factor-1 alpha.
Gallus gallus (Chicken).
Eukaryota, Metazoa; Chordata; Craniata; Vert
Archosauria; Aves; Neognathae; Galliformes;
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Read L.R., Cumberbatch J., Sharif S.;
"Characterization of Chicken SDF-1.";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY451855; AAR88102.1; -.
SEQUENCE 89 AA; 10104 MW; 21E53D121A557965 CRC64;
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